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OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:12 ; Search time 72 Seconds  
(without alignments)  
2281.917 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424  
Sequence: 1 MRSLSARSFLERLEARGG.....NLRIGRPKGRPPPAETRW 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2424	100.0	462	7	ADM29326 Human nov
2	2411	99.5	458	2	AAW49908 Human bra
3	1770.5	73.0	453	2	AAW37254 Novel non
4	1764.5	72.8	353	7	ADC99051 Human KPP
5	1754.5	72.4	453	2	AAW49906 Rat prote
6	1598.5	65.9	327	8	ADK71870 Human kin
7	830	34.2	155	2	AAW37255 Partial h
8	755.5	31.2	802	2	AAW28654 Murine Cy
9	755.5	31.2	802	7	ADL16246 Mouse pro
10	727.5	30.0	807	2	AAW89247 Human PTP
11	726.5	30.0	799	4	AAW78623 Human tyr
12	710	29.3	773	5	ABW57374 Mouse isc
13	709	28.2	780	3	AAW67252 Human pro
14	709	28.2	780	7	ADL16222 Human pro
15	709	28.2	780	7	ADL16220 Human pro
16	709	28.2	780	8	ADH77483 Human PTP
17	709	29.2	780	8	AAW28653 Human Cyt
18	708	29.2	692	2	AAW28653 Human Cyt
19	708	29.2	780	4	AAW51205 Human PTP
20	708	28.2	808	2	AAW28652 Human Cyt
21	705.5	29.1	782	7	ADL16228 Rat prote
22	705	29.1	775	3	AAW67250 Mouse pro
23	703	29.0	780	7	ADL16226 Mouse pro
24	700	28.9	780	4	AAW51201 Human PTP
25	699	28.8	780	3	AAW67253 Human mut

26	698	28.8	780	4	AAW51202 Human PTP
27	695	28.7	775	3	AAW67251 Mutant mo
28	665	27.4	312	4	AAW78281 Human PTP
29	658	27.1	253	4	AAW59383 Human pro
30	529	21.8	237	7	ADC64297 Human SID
31	523	21.6	235	5	ADL17283 Polypepti
32	493.5	20.4	313	4	AAW78277 Human SAP
33	491.5	20.3	1093	6	ABR43689 Human tyr
34	491.5	20.3	1118	6	ABR43688 Human tyr
35	489.5	20.2	1115	8	ADN12200 Human Sap
36	486.5	20.1	255	4	AAW59379 Human pro
37	485	20.0	1705	5	ABW52348 Protein r
38	482.5	19.9	613	7	ADL16248 Rat prote
39	474.5	19.6	624	8	ADH50798 Human SHP
40	474	19.6	1711	2	AAW70506 Osteoste
41	474	19.6	1711	5	ABW52349 Protein r
42	468	19.3	274	4	AAW59385 Protein t
43	467	19.3	595	2	AAW99312 Human SH-
44	464	19.1	1711	2	AAW70507 Mutant os
45	463.5	19.1	341	4	AAW78283 PTP1. 12/

ALIGNMENTS

RESULT 1  
ADM29326  
ID ADM29326 standard; protein; 462 AA.

XX ADM29326;  
AC  
XX 20-MAY-2004 (first entry)  
XX  
XX Human novel protein NOV1a.  
XX  
XX human; novel protein; NOV; cancer; immune associated disorder.  
XX Homo sapiens.  
XX WO2003064628-A2.  
XX  
XX PD 07-AUG-2003.  
XX  
XX PF 03-FEB-2003; 2003WO-US003401.  
XX  
XX 01-FEB-2002; 2002US-0353287P.  
XX 01-FEB-2002; 2002US-0353301P.  
XX 12-FEB-2002; 2002US-0356371P.  
XX 12-FEB-2002; 2002US-0356424P.  
XX 13-FEB-2002; 2002US-0356531P.  
XX 20-FEB-2002; 2002US-0358239P.  
XX 26-FEB-2002; 2002US-0359603P.  
XX 27-FEB-2002; 2002US-0359848P.  
XX 15-MAR-2002; 2002US-0359860P.  
XX 22-MAR-2002; 2002US-0365049P.  
XX 17-MAY-2002; 2002US-0381666P.  
XX 18-JUN-2002; 2002US-0389531P.  
XX 19-JUN-2002; 2002US-0389510P.  
XX 02-JUL-2002; 2002US-0393265P.  
XX 07-AUG-2002; 2002US-0401825P.  
XX 09-AUG-2002; 2002US-0402395P.  
XX 12-AUG-2002; 2002US-0402867P.  
XX 23-AUG-2002; 2002US-0405401P.  
XX 23-AUG-2002; 2002US-0405820P.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Alsobrook JP, Bader JS, Berghs C, Casman SJ;  
PI Catterton E, Chaudhuri A, Edinger SR, Ellerman K, Gerlach VL;  
PI Gorman L, Guo X, Herrmann JL, Ji W, Khrantsov NV, Li L, Miller CE;  
PI Ort T, Patturejan M, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;

PI Spytek KA, Vernet CAM, Zhong H, Zhong M;  
 XX WPI; 2003-646149/61.  
 DR N-PSDB; ADM29325.  
 XX  
 XX New NOVX polypeptide, useful for the manufacture of a medicament for  
 PT treating e.g., cancer or immune associated disorders.  
 PT  
 XX  
 XX Claim 1; SEQ ID NO 70; 606pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequences of novel  
 CC human proteins (NOV proteins). The DNA and protein sequences of the  
 CC invention are useful for the manufacture of a medicament for treating a  
 CC syndrome associated with a human disease comprising a pathology  
 CC associated with the protein, such as: cancer or immune associated  
 CC disorders. The present amino acid sequence represents a NOV protein of  
 CC the invention.  
 CC  
 XX Sequence 462 AA;  
 XX  
 Query Match 100.0%; Score 2424; DB 7; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-222; Indels 0; Gaps 0;  
 Matches 458; Conservative 0; Mismatches 0;  
 QY 1 MRSLSARSFLERLEARGREGAVLAGFSDIQCASAAWKADGVCSTVAGSRPENVRKN 60  
 DB 1 MRSLSARSFLERLEARGREGAVLAGFSDIQCASAAWKADGVCSTVAGSRPENVRKN 60  
 QY 61 RYKDVLPYQOTRVILSLLOEGHSDYINGNFRGVDSGLAYIATCGPLPHTLLDFWRLVW 120  
 DB 61 RYKDVLPYQOTRVILSLLOEGHSDYINGNFRGVDSGLAYIATCGPLPHTLLDFWRLVW 120  
 QY 121 EFGVKVILMACREIENGRKRCERYWAQOEPLQTLGFCITLKEKWLNEDIMRLTKVTF 180  
 DB 121 EFGVKVILMACREIENGRKRCERYWAQOEPLQTLGFCITLKEKWLNEDIMRLTKVTF 180  
 QY 181 QKESRSVYQIYMSWPDGVPSSPDHMLAMVEARLRQSGPEPLCVHCSAGCGRTGVLC 240  
 DB 181 QKESRSVYQIYMSWPDGVPSSPDHMLAMVEARLRQSGPEPLCVHCSAGCGRTGVLC 240  
 QY 241 TVDYVRQLLTQMIIPDFSLFDVWLKQRKORAAVQTEEQRYFLYHTVAQMFCSLQNAS 300  
 DB 241 TVDYVRQLLTQMIIPDFSLFDVWLKQRKORAAVQTEEQRYFLYHTVAQMFCSLQNAS 300  
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSRSISVPGSPGHAMADTYAEQKR 360  
 DB 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSRSISVPGSPGHAMADTYAEQKR 360  
 QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADQSPAG 420  
 DB 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADQSPAG 420  
 QY 421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458  
 DB 421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458  
 RESULT 2  
 AAW49908  
 ID AAW49908 standard; protein; 458 AA.  
 XX  
 AC AAW49908;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 XX Human brain derived phosphatase 1 (BDP-1).  
 DE  
 XX Brain derived phosphatase 1; BDP-1; human; receptor;  
 KW protein tyrosine phosphatase; signal transduction; therapy; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9748723-A2.  
 FN

XX 24-DEC-1997.  
 DD 17-JUN-1997; 97WO-IB000946.  
 XX  
 XX 17-JUN-1996; 96US-0019629P.  
 PR 09-AUG-1996; 96US-0023485P.  
 PR 13-NOV-1996; 96US-0030860P.  
 PR 15-NOV-1996; 96US-0030964P.  
 PR 19-DEC-1996; 96US-0034286P.  
 XX  
 XX (PLAC') MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 PA  
 XX Ullrich A, Kharitonov AI, Aoki N, Wang HY, Chen Z, Nayler O;  
 PI Kim YH;  
 PI Kim YH;  
 XX WPI; 1998-120302/11.  
 DR N-PSDB; AAV17099.  
 XX  
 XX New phosphatase and kinase enzyme(s) - useful in the diagnosis and  
 PT treatment of signal transduction disorders.  
 PT  
 XX Claim 11; Fig 3a-d; 138pp; English.  
 PS  
 XX This polypeptide comprises a novel human protein tyrosine phosphatase  
 CC (PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed  
 CC in most tissues and cell lines at basal level, but expressed high in  
 CC epithelium origin cell lines and cancer cell lines. The amino acid  
 CC sequence was deduced from a cDNA clone (see AAV17099) isolated from a  
 CC haematopoietic MEG01 cDNA library. The invention relates to novel  
 CC proteins (see AAW49908-14) involved in cellular signal transduction and  
 CC to the nucleic acids (see AAV17097-99) coding for them, and provides  
 CC vectors, host cells, purified recombinant proteins, methods for  
 CC identifying compounds that activate or inhibit the novel proteins, as  
 CC well as methods for the diagnosis and treatment of diseases associated  
 CC with the novel proteins  
 CC  
 XX Sequence 458 AA;  
 SQ  
 Query Match 99.5%; Score 2411; DB 2; Length 458;  
 Best Local Similarity 99.8%; Pred. No. 1.2e-220;  
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MRSLSARSFLERLEARGREGAVLAGFSDIQCASAAWKADGVCSTVAGSRPENVRKN 60  
 DB 1 MRSLSARSFLERLEARGREGAVLAGFSDIQCASAAWKADGVCSTVAGSRPENVRKN 60  
 QY 61 RYKDVLPYQOTRVILSLLOEGHSDYINGNFRGVDSGLAYIATCGPLPHTLLDFWRLVW 120  
 DB 61 RYKDVLPYQOTRVILSLLOEGHSDYINGNFRGVDSGLAYIATCGPLPHTLLDFWRLVW 120  
 QY 121 EFGVKVILMACREIENGRKRCERYWAQOEPLQTLGFCITLKEKWLNEDIMRLTKVTF 180  
 DB 121 EFGVKVILMACREIENGRKRCERYWAQOEPLQTLGFCITLKEKWLNEDIMRLTKVTF 180  
 QY 181 QKESRSVYQIYMSWPDGVPSSPDHMLAMVEARLRQSGPEPLCVHCSAGCGRTGVLC 240  
 DB 181 QKESRSVYQIYMSWPDGVPSSPDHMLAMVEARLRQSGPEPLCVHCSAGCGRTGVLC 240  
 QY 241 TVDYVRQLLTQMIIPDFSLFDVWLKQRKORAAVQTEEQRYFLYHTVAQMFCSLQNAS 300  
 DB 241 TVDYVRQLLTQMIIPDFSLFDVWLKQRKORAAVQTEEQRYFLYHTVAQMFCSLQNAS 300  
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSRSISVPGSPGHAMADTYAEQKR 360  
 DB 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSRSISVPGSPGHAMADTYAEQKR 360  
 QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADQSPAG 420  
 DB 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADQSPAG 420  
 QY 421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458  
 DB 421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458

Db 421 SGAYEDVAGGAQTGGGLGNLRIGRPGKPRDPPAEWTRV 458

RESULT 3

AAW37254  
ID AAW37254 standard; protein; 453 AA.

XX AC AAW37254; \

XX DT 09-APR-1998 (first entry)

XX DE Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.

XX KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;  
KW PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;  
KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;  
KW stem cell differentiation.

XX OS Mus sp.

XX PH Key Location/Qualifiers

XX FT Domain 6..303

XX FT Active-site /note= "tyrosine phosphatase domain"

XX FT /note= "phosphorylated by protein kinases A and C; also  
appears to negatively regulate PTPase activity"

XX FT Active-site /note= "active site cysteine residue"

XX FT Region 312..428

XX FT Region /note= "Pro, Ser and Thr rich region"

XX FT Region 430..450

XX FT /note= "homologous to a nuclear localization signal found  
on murine PTP PEP"

WO9735019-A1.

25-SEP-1997.

17-MAR-1997; 97WO-US005278.

22-MAR-1996; 96US-00620526.

(GETH ) GENENTECH INC.

Lasky LA, Cheng J;

WPI; 1997-480224/44.

N-PSDB; AAV03112.

Haematopoietic stem cell non-receptor protein tyrosine phosphatase -  
useful for expansion of undifferentiated stem cells in cell culture.

Claim 9; Fig 1; 66pp; English.

The present sequence represents a novel murine non-receptor protein  
tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein  
is predominantly expressed in early hematopoietic stem cells (HSCs) or  
progenitor cells, and lacks expression in adult tissues. The protein has  
a N-terminal tyrosine phosphatase domain, followed by a region rich in  
serine, threonine and proline and a C-terminal region of about 15-25  
amino acids which is rich in basic amino acid residues. The protein is  
capable of tyrosine dephosphorylation in hematopoietic progenitor cells,  
and functional derivatives of such native tyrosine phosphatases. The  
phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or  
progenitor cell can be used in an assay for the identification of PTP HSC  
antagonists or agonists. The antagonist can be used to induce the  
differentiation of stem cells, such as undifferentiated malignant  
hematopoietic cells, e.g. leukaemia cells, which may facilitate their  
treatment. The PTP HSC or an agonist antibody against the PTP HSC can be  
used for the expansion of undifferentiated stem cells in cell culture  
(this allows expansion of HSC prior to autologous or heterologous bone  
marrow transplantation), while the agonist antibody along with a  
hematopoietic growth factor can be used for the expansion of

CC undifferentiated stem cells in vivo

XX Sequence 453 AA;

Query Match 73.0%; Score 1770.5; DB 2; Length 453;  
Best Local Similarity 74.7%; Pred. No. 1.4e-159;  
Matches 343; Conservative 32; Mismatches 77; Indels 7; Gaps 2;

QY 1 MSRLDSARSFLERLEARGGREGAVLAGBPSDIQACSAANKADGVCSTVAGSPENVRKN 60  
DB 1 MSRHTLVRSFLEQLEARDYREGAIFVRFSDIKARSVANKSEGVCSKAGSLGNTNKN 60

QY 61 RYKDLVPYDQTRVILSLQEGHSDYINGNPIRGVDGSLAYIATQGPLHTLLDFWRLVW 120  
DB 61 RYKDWAYDETRVILSLQEGHGNINANFIRGIDGQAYIATQGPLHTLLDFWRLVW 120

QY 121 EFGVKVILMACREJENGRKCYWAOBLOTLGFCITLKEKLNEDIMLTTLKVT 180  
DB 121 EFGVKVILMACQETENGRKCYWAOBLOTLGFCITLKEKLNEDIMLTTLKVT 180

QY 181 QKESRSVYQLQYMSWPDGRGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240  
DB 181 QKESRSVYQLQYMSWPDGRGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240

QY 241 TVDYVRQLLLTQMPPDFSLFDVILKMRKQPPAAVOTEEQYRFLYHTVAQFCSTLQNAS 300  
DB 241 AVDYVRQLLLTQMPPDFSLFDVILKMRKQPPAAVOTEEQYRFLYHTVAQFCSTLQNAS 300

QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360  
DB 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360

QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAQPOAHAEADARGTLP-GRVPADQSPA 419  
DB 361 GASAGTGPAPRPTST-----DTPIYSQVAPRAQRPVAHTEDACGTTALRRVPADQNS 414

QY 420 GSGAYEDVAGGAQTGGGLGNLRIGRPGKPRDPPAEWTRV 458  
DB 415 GPDAYEEVTGAGTGGGLGNLRIGRPGKPRDPPAEWTRV 453

RESULT 4

ADC99051  
ID ADC99051 standard; protein; 353 AA.

XX AC ADC99051;

XX DT 01-JAN-2004 (first entry)

XX DE Human KPP protein - SEQ ID 4.

XX KW anti-HIV; anti-allergic; anti-inflammatory; antianaemic; anti-parkinsonian;  
KW neotropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;  
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
KW osteopathic; antihistaminic; antiparasitic; antihelminthic; antipsoriatic;  
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
KW cancer; developmental; mental retardation; neurological;  
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
KW helminthic infection; transgenic; gene therapy; human; enzyme.

XX OS Homo sapiens.

XX PN WO2003033680-A2.

XX PD 24-APR-2003.

XX PF 17-OCT-2002; 2002WO-US033723.

XX PR 19-OCT-2001; 2001US-0345474P.

PR 02-NOV-2001; 2001US-0343910P.  
 PR 13-NOV-2001; 2001US-0333098P.  
 PR 16-NOV-2001; 2001US-0332424P.  
 PR 30-NOV-2001; 2001US-0334288P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
 PI Emerling BM, Forsythe IV, Gandhi AR, Gorvad AE, Griffin JA;  
 PI Gururajan R, Hafalia AUA, Khan FA, Lal PG, Lee EA, Lee SY;  
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 PI Zebajadian Y;  
 XX  
 XX WPI; 2003-403214/38.  
 DR N-PSDB; ADC99103.  
 XX  
 XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX  
 PS Claim 1; SEQ ID NO 4; 424pp; English.  
 XX  
 XX The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.  
 XX  
 XX Sequence 353 AA;  
 SQ  
 Query Match 72.8%; Score 1764.5; DB 7; Length 353;  
 Best Local Similarity 75.9%; Pred. No. 3.7e-159; Mismatches 2; Indels 109; Gaps 2;  
 Matches 349; Conservative 0;  
 QY 1 MSRLSDARSFLERLEARGREGAVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60  
 DB |||||  
 QY 1 MSRLSDARSFLERLEARGREGAVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60  
 DB |||||  
 QY 61 RYKDVLPYQCTVILSLLOEGHSDYINGNFTIRGVDGSLAYIATOGPLPHLLDFWRLVW 120  
 DB |||||  
 QY 121 EFGVKVILMACREIENGRCRYERWAQEQPIQTGLFCTITIKERKWLNEDIMRLTKVTF 180  
 DB |||||  
 QY 181 QKESRSVYQLQWSPDRGVPSPDHMLAWBEARLQSGPEPLCVHCSAGCGRTGVLG 240  
 DB 74 QKESRSVYQLQWSPDRGVPSPDHMLAWBEARLQSGPEPLCVHCSAGCGRTGVLG 133  
 QY 241 TVDYVYRQLLTLQMI PDFSLFDVLMKQRQAPAAVQTEBQVRFYHTVAQMFCSLQNAS 300  
 DB 134 TVDYVYRQLLTLQMI PDFSLFDVLMKQRQAPAAVQTEBQVRFYHTVAQMFCSLQNAS 193  
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVILRSISVPGSPGHAMADTYAEQKR 360  
 DB 194 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVILRSISVPGSPGHAMADTYAVQKR 253  
 QY 361 GAPAGAGSGTQ--TGTTGARGAAEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSP 418  
 DB 254 GAPAGAGSGTQ--TGTTGARGAAEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSP 313

QY 419 AGSGAYEDVAGGAQTGGLGNLIRIGRPKGRDPPPAEWTRV 458  
 DB 314 AGSGAYEDVAGGAQTGGLGNLIRIGRPKGRDPPPAEWTRV 353  
 RESULT 5  
 AAW49906  
 ID AAW49906 standard; protein; 453 AA.  
 AC AAW49906;  
 XX 20-JUL-1998 (first entry)  
 DT  
 XX Rat protein tyrosine phosphatase PRP20.  
 DE  
 XX Protein tyrosine phosphatase; PTP20; rat; signal transduction;  
 KW cell differentiation; cancer; neural injury; therapy.  
 XX  
 XX Rattus sp.  
 OS  
 XX WO9748723-A2.  
 PN  
 XX 24-DEC-1997.  
 PD  
 XX 17-JUN-1997; 97WO-IB000946.  
 PF  
 XX 17-JUN-1996; 96US-0019629P.  
 PR 09-AUG-1996; 96US-0023485P.  
 PR 13-NOV-1996; 96US-0030860P.  
 PR 15-NOV-1996; 96US-0030964P.  
 PR 19-DEC-1996; 96US-0034286P.  
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 PA  
 XX Ullrich A, Kharitonov AI, Aoki N, Wang HY, Chen Z, Nayler O;  
 PI Kim YW;  
 PI  
 XX WPI; 1998-120302/11.  
 DR N-PSDB; AAV17097.  
 XX  
 XX New phosphatase and kinase enzyme(s) - useful in the diagnosis and  
 PT treatment of signal transduction disorders.  
 PT  
 XX Claim 11; Fig 1a-b; 138pp; English.  
 XX  
 XX This polypeptide comprises a novel rat protein tyrosine phosphatase,  
 CC designated PTP20, that regulates growth factor stimulation of cellular  
 CC differentiation. Its amino acid sequence was deduced from a cDNA clone  
 CC (see AAV17097) isolated from a rat phaeochromocytoma PC12 cDNA library by  
 CC PCR amplification using primers based on consensus sequences (see  
 CC AAW49915-16) of known PTPs. The invention relates to novel proteins (see  
 CC AAW49906-14) involved in cellular signal transduction and to the nucleic  
 CC acids (see AAV17097-99) coding for them, and provides vectors, host  
 CC cells, purified recombinant proteins, methods for identifying compounds  
 CC activate or inhibit the novel proteins, as well as methods for the  
 CC diagnosis and treatment of diseases associated with the novel proteins.  
 CC For PTP20, activators may act as anti-cancer therapeutics that stimulate  
 CC cell differentiation rather than proliferation, while inhibitors may be  
 CC useful for treating neural injuries by delaying the differentiation of  
 CC transplanted neuronal stem cells until they are firmly grafted  
 XX  
 SQ Sequence 453 AA;  
 Query Match 72.4%; Score 1754.5; DB 2; Length 453;  
 Best Local Similarity 74.5%; Pred. No. 4.8e-158;  
 Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;  
 QY 1 MSRLSDARSFLERLEARGREGAVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60  
 DB |||||  
 QY 1 MSRLSDARSFLERLEARGREGAVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60  
 DB |||||  
 QY 61 RYKDVLPYQCTVILSLLOEGHSDYINGNFTIRGVDGSLAYIATOGPLPHLLDFWRLVW 120  
 DB |||||

Db 61 RYKDVVPYBETRVILSLQEGHGYDINANFIRGTGSGQAYIATOGPLPHTLLDFWRLVW 120  
 QY 121 EFGVKVILMACREIENGKRCERYWAQOEPLQTLGFCITLKEKWLNEIMLRLTKVTF 180  
 Db 121 EFGIKVILMACOBTENGKRCERYWAQOEPLQAGFCITLTKETALTSITLRLQVTF 180  
 QY 181 QKESRSVYLOQYMSWPDGVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVL 240  
 Db 181 QKESRPVHQLOQYMSWPDGVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVL 240  
 QY 241 TVDYVRQLLLTQMIPDFSLFDVLMKMRQKRAAQAQTEEQVRFVHTVAQMFCSLQNAS 300  
 Db 241 AVDYVRQLLLTQIPDNFSLFVLMEMRKORPAQAQTEEQVRFVHTVAQMFCSLQNAS 300  
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSISVPGSPGHAMADTYAEQKR 360  
 Db 301 PLYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSISVPGSPGHAMADTYAEQKR 360  
 QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPEAQPAGAHADARGTLPGRVADQSP 419  
 Db 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQTGTALGRVPADENPS 414  
 QY 420 GSGAYEDVAGGAGTGGGLGNLRIGRPKGRDPPAEWTRV 458  
 Db 415 GPDAYEEDVAGGAGTGGGLGNLRIGRPKGRDPPAEWTRV 453

RESULT 6

ADK71870

ID ADK71870 standard; protein; 327 AA.

XX ADK71870;

AC ADK71870;

XX 20-MAY-2004 (first entry)

XX Human kinase and phosphatase KPP-47 protein.

XX human: kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;

XX hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;

XX antiallergic; antiaschmatic; immunosuppressive; antithyroid;

XX dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal;

XX neuroprotective; osteopathic; antiarthritic; uteropathic; ophthalmological;

XX antitumetic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;

XX antipsoriatic; haemostatic; cytostatic; antilipemic; antiparasitic;

XX antihelminthic; antibacterial; virucide; procoagulant; fungicide;

XX cardiovascular disease; immune system; neurological; growth; development;

XX cell proliferation; viral; bacterial; fungal; parasitic; protozoan;

XX helminthic infection; transgenic; gene therapy; enzyme.

XX Homo sapiens.

XX WO2004018641-A2.

XX 04-MAR-2004.

XX 25-AUG-2003; 2003WO-US026635.

XX 26-AUG-2002; 2002US-0406172P.

XX 25-SEP-2002; 2002US-0413910P.

XX 27-SEP-2002; 2002US-0414296P.

XX 11-OCT-2002; 2002US-0417821P.

XX (INCY-) INCYTE CORP.

XX Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;

XX Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;

XX Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;

XX Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;

XX Murage J;

XX WFI; 2004-226830/21.

XX N-PSDB; ADK71929.

PT New human kinases and phosphatases, useful for diagnosing, treating or  
 PT preventing arteriosclerosis, hypertension, AIDS, allergy, multiple  
 PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer  
 PT or hepatitis.

XX Claim 1; SEQ ID NO 47; 347pp; English.

PS The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The polypeptide of the invention  
 CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive,  
 CC vasotropic, antiinflammatory, antianginal, anti-HIV, antiallergic,  
 CC antidiabetic, immunosuppressive, antithyroid, dermatological,  
 CC antipsoriatic, nephrotropic, antigout, gastrointestinal, neuroprotective,  
 CC osteopathic, antiarthritic, uteropathic, ophthalmological, antiparasitic,  
 CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antiparasitic,  
 CC haemostatic, cytostatic, antilipemic, antiparasitic, antihelminthic,  
 CC antibacterial, virucide, protozoacidal, and fungicidal activities. The  
 CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and  
 CC antagonists may be useful for diagnosing, treating or preventing  
 CC disorders such as cardiovascular diseases, immune system disorders,  
 CC neurological disorders, disorders affecting growth and development, cell  
 CC proliferative disorders and viral, bacterial, fungal, parasitic, of the  
 CC protozoan or helminthic infections. Furthermore, the molecules of the  
 CC invention may be useful for creating transgenic animals to model human  
 CC disease and during gene therapy. The current sequence is that of a human  
 CC KPP protein of the invention.

XX SQ Sequence 327 AA;

Query Match 65.9%; Score 1598.5; DB 8; Length 327;

Best Local Similarity 69.8%; Fred. No. 2.3e-143;

Matches 321; Conservative 0; Mismatches 4; Indels 135; Gaps 3;

QY 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAAMKADGVCSTVAGSRDENVRKN 60

Db 1 MSRSLSARSFLERLEARGREGAVLAGEFS----- 31

QY 61 RYKDVLPDQTRVILSLQEGHSDYINGNPIRGVDSLAYIATOGPLPHTLLDFWRLVW 120

Db 32 ----- 31

QY 121 EFGVKVILMACREIENGKRCERYWAQOEPLQTLGFCITLKEKWLNEIMLRLTKVTF 180

Db 32 -----KRCERYWAQOEPLQTLGFCITLKEKWLNEIMLRLTKVTF 73

QY 181 QKESRSVYLOQYMSWPDGVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVL 240

Db 74 QKGSRSVYLOQYMSWPDGVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVL 133

QY 241 TVDYVRQLLLTQMIPDFSLFDVLMKMRQKRAAQAQTEEQVRFVHTVAQMFCSLQNAS 300

Db 134 TVDYVRQLLLTQ-----EQYRFVHTVAQMFCSLQNAS 167

QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSISVPGSPGHAMADTYAEQKR 360

Db 168 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGVLSISVPGSPGHAMADTYAEQKR 227

QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPEAQPAGAHADARGTLPGRVADQSP 418

Db 228 GAPAGAGSGTGTGTGARSABEAPLYSKVTPEAQPAGAHADARGTLPGRVADQSP 287

QY 419 AGSGAYEDVAGGAGTGGGLGNLRIGRPKGRDPPAEWTRV 458

Db 288 AGSGAYEDVAGGAGTGGGLGNLRIGRPKGRDPPAEWTRV 327

RESULT 7

AAW37255

ID AAW37255 standard; protein; 155 AA.

XX AAW37255;

XX AAW37255;

DT 09-APR-1998 (first entry)

```

XX DE Partial human non-receptor tyrosine phosphatase.
XX KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
XX PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
XX KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
XX KW stem cell differentiation.
XX CS Homo sapiens.
XX PN WO9735019-A1.
XX PD 25-SEP-1997.
XX PF 17-MAR-1997; 97WO-US005278.
XX PR 22-MAR-1996; 96US-00620526.
XX PA (GETH ) GENENTECH INC.
XX PI Lasky LA, Cheng J;
XX DR WPI; 1997-480224/44.
XX DR N-PSDB; AAV03128.
XX PT Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
XX PT useful for expansion of undifferentiated stem cells in cell culture.
XX PS Claim 9; Fig 8; 66pp; English.
XX CC The present sequence represents a partial human non-receptor protein
XX CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
XX CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
XX CC progenitor cells, and lacks expression in adult tissues. The protein has
XX CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
XX CC serine, threonine and proline and a C-terminal region of about 15-25
XX CC amino acids which is rich in basic amino acid residues. The protein is
XX CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
XX CC and functional derivatives of such native tyrosine phosphatases. The
XX CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
XX CC progenitor cell can be used in an assay for the identification of PTP HSC
XX CC antagonists or agonists. The antagonist can be used to induce the
XX CC differentiation of stem cells, such as undifferentiated malignant
XX CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
XX CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
XX CC used for the expansion of undifferentiated stem cells in cell culture
XX CC (this allows expansion of HSC prior to autologous or heterologous bone
XX CC marrow transplantation), while the agonist antibody along with a
XX CC hematopoietic growth factor can be used for the expansion of
XX CC undifferentiated stem cells in vivo
XX SQ Sequence 155 AA;
XX CC Query Match 34.2%; Score 830; DB 2; Length 155;
XX CC Best Local Similarity 100.0%; Pred. No. 1.5e-70;
XX CC Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 17 ARGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDLVPYDQTRVILS 76
XX DB 1 ARGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDLVPYDQTRVILS 60
XX QY 77 LQOEGHSDYINGNFRGVGDSGLAVIATQGPLPHLLDFWRLVWFGVKVILMACREIEN 136
XX DB 61 LQOEGHSDYINGNFRGVGDSGLAVIATQGPLPHLLDFWRLVWFGVKVILMACREIEN 120
XX QY 137 GRKRCERYWAQOEPLQTLGFCITILKEKWLNEDI 171
XX DB 121 GRKRCERYWAQOEPLQTLGFCITILKEKWLNEDI 155
XX RESULT 8
XX AAY28654
XX ID AAY28654 standard; protein; 802 AA.

```

```

XX AC AAY28654;
XX DT 01-OCT-1999 (first entry)
XX DE Murine Cytoplasmic phosphatase, Z70PEP protein.
XX KW Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell;
XX KW intracellular tyrosine phosphatase; Pfrase; lymphocyte; murine;
XX KW protein tyrosine kinase; PTKs; immunosuppressant; PEST sequence;
XX KW T cell antigen receptor signalling; autoimmune disease; transplant;
XX KW cytokine receptor signalling.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT Domain 27..288
XX FT /label= PTPase domain
XX FT /note= "Catalytic protein tyrosine phosphatase domain"
XX FT Binding-site 613..621
XX FT /label= SH3 binding site
XX FT /note= "SH3 binding site"
XX FT Binding-site 689..695
XX FT /label= SH3 binding site
XX FT /note= "SH3 binding site"
XX FT Binding-site 790..798
XX FT /label= SH3 binding site
XX FT /note= "SH3 binding site"
XX FT W09936548-A1.
XX PD 22-JUL-1999.
XX PF 18-JAN-1999; 99WO-CA000038.
XX PR 16-JAN-1998; 98CA-02220853.
XX PA (HSCR-) HSC RES & DEV LP.
XX PI Roifman CM;
XX PF WPI; 1999-444404/37.
XX CC New nucleic acid encoding intracellular tyrosine phosphatase and related
XX CC proteins, used to modulate signaling through T cells, particularly as
XX CC immunosuppressant.
XX PS Disclosure; Page 63-64; 105pp; English.
XX CC The present protein sequence is that of the murine phosphatase, Z70PEP
XX CC that has a single catalytic domain. The non-catalytic portion of the
XX CC phosphatase contains unique sequences, including five PEST sequences rich
XX CC in Pro, Glu or Asp, Ser and Thr. Z70PEP shares about 70% sequence
XX CC identity with the human cytoplasmic phosphatase Lyp1. Lyp proteins are
XX CC important for regulation of T cell antigen and cytokine receptor
XX CC signalling and for early and late stages of T cell differentiation.
XX CC Z70PEP has immunosuppressive activity. Compounds that increase expression
XX CC of Lyp protein can be used as immunosuppressive agents to reduce or
XX CC prevent T cell activation or proliferation, to control thymocyte
XX CC differentiation, to treat autoimmune diseases and transplant situations
XX SQ Sequence 802 AA;
XX CC Query Match 31.2%; Score 755.5; DB 2; Length 802;
XX CC Best Local Similarity 44.0%; Pred. No. 2.1e-62;
XX CC Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;
XX QY 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDLVPYDQTRVILSLQEGHSDY 86
XX DB 25 ASEFLKRCSTKYKADKIYPTTVACRPKNIKKNRYKDLVSHLSVLSLTSDSDSY 84
XX QY 87 INGNFRGVGDSGLAVIATQGPLPHLLDFWRLVWFGVKVILMACREIENGKRCERYWA 146

```

Db 85 INASFIKGVGPKAYIATQGPLSTLLDFWRMIWEYRILVIMVACMEFEMGKKKERYWA 144  
QY 147 QEQE-PLQTGLFCITLIKELWLNEDIMLRTLVTFQKESRSVVOLOYMSWDRGVSPSPD 205  
Db 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTKAKFNNEIRIYQFHYKNWPDHVPSSID 203  
QY 206 HMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVROLLLTQMIIPDFSLFDVVL 265  
Db 204 PILQLIWMRCYQEDDCVPICHCSAGCGRTGVCIVADYTWMLLKDGIIIPKFSVENLIQ 263  
QY 266 KMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDALFLRTPQA 325  
Db 264 EMRTQPSLVQTEQYELVYSVLELF-----KRMVDVSDNHLG-----REIOA 308  
QY 326 LLAIPRPPGGVLSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTQTGTGTG 377  
Db 309 QCSIFE-----QSLTVEADSCPLDLPKNAMRDVKTTHQSKQGAESTGSSSLGLRTS 362  
QY 378 ARSAEE 383  
Db 363 TWNAEE 368

RESULT 9  
ADL16246  
ID ADL16246 standard; protein; 802 AA.  
XX  
AC ADL16246;  
DT 06-MAY-2004 (first entry)  
DE Mouse protein tyrosine phosphatase #7.  
KW cytosolic; immunosuppressive; antiallergic;  
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;  
KW inducible signalling pathway; cell proliferation; cancer;  
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;  
KW cell-cycle abnormality.  
OS Mus musculus.  
XX  
FN WO2003068984-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-EP001446.  
XX  
XX 13-FEB-2002; 2002US-0356810P.  
PR 12-FEB-2003; 2003US-00366547.  
XX  
FA (COLD-) COLD SPRING HARBOR LAB.  
FA (CEPT-) CEPTYR INC.  
XX  
PI Tonks NK, Tzu-Ching M, Cool DE;  
XX  
XX WPI; 2003-712572/67.  
DR N-PSDB; ADL16245.  
XX

Identifying reversibly oxidized protein tyrosine phosphatase, useful in screening for specific modulators, potential agents for treating e.g. cancer or autoimmune disease.  
PS Disclosure; SEQ ID NO 95; 238pp; English.  
XX  
XX The invention relates to a method for identifying a protein tyrosine phosphatase (PTP) that is reversibly oxidized in a cell by: (i) subjecting a sample, including a cell that contains at least one PTP, to conditions that cause reversible oxidation of PTP; (ii) isolating PTP anaerobically, in presence of a sulphydryl-reactive agent (II) that irreversibly modifies the thiol group of an invariant Cys in the active site of PTP; and (iii) determining, under reducing conditions, the level of dephosphorylation, caused by PTP, of a labelled substrate (III), where dephosphorylation indicates that an active PTP is present. . No details

CC of tests for these activities are given. The method is used to identify reversibly oxidized PTP, also to identify agents that: (a) reversibly modify such PTP; or (b) alter inducible signalling pathways in which PTP are involved. These agents are potentially useful, in human or veterinary medicine, for treating abnormal cell proliferation or growth (cancer); guest vs. host disease; autoimmune diseases; allergy or other immunosuppressed states; metabolic disorders and cell-cycle abnormalities. This sequence represents one of the PTP enzyme of the invention.  
XX  
SQ Sequence 802 AA;

Query Match 31.2%; Score 755.5; DB 7; Length 802;  
Best Local Similarity 44.0%; Pred. No. 2.1e-62;  
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;  
QY 27 AGEFSDIACSAAMKADGVCSTVAGSRPENVRKNRYKDLVLPYDQTRVILSLQEGHSDY 86  
Db 25 ASEFLKLRQSTKYKADKIYFTTVAQRPKNIKKNRYKDLIPYDHSLSVLSLTDESSY 84  
QY 87 INGNFIRGVDSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146  
Db 85 INASFIKGVGPKAYIATQGPLSTLLDFWRMIWEYRILVIMVACMEFEMGKKKERYWA 144  
QY 147 QEQE-PLQTGLFCITLIKELWLNEDIMLRTLVTFQKESRSVVOLOYMSWDRGVSPSPD 205  
Db 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTKAKFNNEIRIYQFHYKNWPDHVPSSID 203  
QY 206 HMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVROLLLTQMIIPDFSLFDVVL 265  
Db 204 PILQLIWMRCYQEDDCVPICHCSAGCGRTGVCIVADYTWMLLKDGIIIPKFSVENLIQ 263  
QY 266 KMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDALFLRTPQA 325  
Db 264 EMRTQPSLVQTEQYELVYSVLELF-----KRMVDVSDNHLG-----REIOA 308  
QY 326 LLAIPRPPGGVLSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTQTGTGTG 377  
Db 309 QCSIFE-----QSLTVEADSCPLDLPKNAMRDVKTTHQSKQGAESTGSSSLGLRTS 362  
QY 378 ARSAEE 383  
Db 363 TWNAEE 368

RESULT 10  
AAW89247  
ID AAW89247 standard; protein; 807 AA.  
XX  
AC AAW89247;  
XX  
DT 10-MAR-1999 (first entry)  
XX  
DE Human PTP04.  
XX  
KW PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;  
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;  
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease.  
XX Homo sapiens.  
XX  
XX WO9849317-A2.  
XX  
XX 05-NOV-1998.  
PD 27-APR-1998; 98WO-US008439.  
XX  
XX 28-APR-1997; 97US-0044428P.  
PR 20-MAY-1997; 97US-0047222P.  
PR 11-JUN-1997; 97US-0049477P.  
PR 11-JUN-1997; 97US-0049756P.  
PR 18-JUN-1997; 97US-0049914P.

PR 23-OCT-1997; 97US-006359SP.  
 XX (SUGC-) SUGEN INC.  
 XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;  
 PI Courtneidge SA, App H, Hui TH;  
 PI WPI; 1999-009434/01.  
 DR N-PSDB; AAV81742.  
 XX New nucleic acid encoding specific protein tyrosine phosphatases - useful  
 PT for identifying specific modulators for treatment and prevention of  
 PT cancer and neurodegenerative disease.  
 XX  
 PS Claim 2; Page 151-153; 193pp; English.  
 XX The present invention describes isolated, enriched or purified nucleic  
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The  
 CC present sequence represents human PTP04. The above proteins, other than  
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify  
 CC substances that modulate their activity (i.e. agonists and antagonists,  
 CC including NBP) in vivo or in vitro. These substances are used to treat or  
 CC prevent diseases associated with abnormal signal transduction pathways  
 CC that involve the proteins, particularly cancer (e.g. leukaemia and  
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor  
 CC serine/threonine kinase) are used to promote neuronal survival,  
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's  
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the  
 CC proteins can be used as probes to identify and clone related sequences;  
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene  
 CC therapy (optionally after mutation). Ab are used to determine the  
 CC proteins  
 XX  
 SQ Sequence 807 AA;  
 Query Match 30.0%; Score 727.5; DB 2; Length 807;  
 Best Local Similarity 46.9%; Pred. No. 9.9e-60;  
 Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;  
 QY 27 AGFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLQEGHSDY 86  
 DB 25 ANEFLKLRQSTKYKADKTYPTTVAEKPKNKKRYKDLFPDYSRVLSLTSDESSY 84  
 QY 87 INGNFIRGVDGSLAYIATQGPLHTLLDFWRLVWFGVKVILMACREIENGRKRCERYWA 146  
 DB 85 INANFIKGYGPKAVIATQGPLSTLLDFWRMIWEYSVLIIWVACMEYEMGKKCERYWA 144  
 QY 147 QEQE-PLQGLFCITILKEKWLNEIMLTAKVTQKESRSVYQLQYMSWPDGRGVPSSPD 205  
 DB 145 EPGEMQLFEGPFSVSCAEK-RKSDYIIRTLKVKFNSETRTIYQHYKNWPDHVPSSID 203  
 QY 206 HMLAMVEEARLQGGSGPEPLCVHCSAGCGRTGLCTDVRQLLTQMTIPDFSLFDVVL 265  
 DB 204 PILELWDVRCQEDDSVFCIHCAGCGRTGVCICAIDYTWMLKDGIIPEFVSFLIR 263  
 QY 266 KMKRQRPAAVQTEEQRYFLHYHTVAQMF---CSTLQNASPHYQNIKENCAP 312  
 DB 264 EMRTQPSLVQTEQYELVYNVAVLELFKQMDVIRDKHSGTSGAKHCIP 313  
 RESULT 11  
 AAG78623  
 ID AAG78623 standard; protein; 799 AA.  
 XX AAG78623;  
 AC  
 XX  
 XX 04-DEC-2001 (first entry)  
 DT Human tyrosine phosphatase.  
 DE  
 XX Human; tyrosine phosphatase; hTTP.  
 KW Homo sapiens.  
 XX

XX CN1302899-A.  
 XX 11-JUL-2001.  
 XX 29-OCT-1999; 99CN-00119935.  
 XX 29-OCT-1999; 99CN-00119935.  
 XX (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.  
 PA Ren S, Wu T, Qian B;  
 XX WPI; 2001-550591/62.  
 DR N-PSDB; AAH79342.  
 XX Human protein tyrosine phosphatase and its coding sequence.  
 XX Claim 4; Page 12-13 (Disclosure); 29pp; Chinese.  
 XX The present invention provides the protein and coding sequences of human  
 CC tyrosine phosphatase hTTP. The protein is expressed in human normal  
 CC suprarenal tissue. The present sequence is the protein of the invention  
 XX  
 SQ Sequence 799 AA;  
 Query Match 30.0%; Score 726.5; DB 4; Length 799;  
 Best Local Similarity 46.9%; Pred. No. 1.2e-59;  
 Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;  
 QY 27 AGFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLQEGHSDY 86  
 DB 25 ANEFLKLRQSTKYKADKTYPTTVAEKPKNKKRYKDLFPDYSRVLSLTSDESSY 84  
 QY 87 INGNFIRGVDGSLAYIATQGPLHTLLDFWRLVWFGVKVILMACREIENGRKRCERYWA 146  
 DB 85 INANFIKGYGPKAVIATQGPLSTLLDFWRMIWEYSVLIIWVACMEYEMGKKCERYWA 144  
 QY 147 QEQE-PLQGLFCITILKEKWLNEIMLTAKVTQKESRSVYQLQYMSWPDGRGVPSSPD 205  
 DB 145 EPGEMQLFEGPFSVSCAEK-RKSDYIIRTLKVKFNSETRTIYQHYKNWPDHVPSSID 203  
 QY 206 HMLAMVEEARLQGGSGPEPLCVHCSAGCGRTGLCTDVRQLLTQMTIPDFSLFDVVL 265  
 DB 204 PILELWDVRCQEDDSVFCIHCAGCGRTGVCICAIDYTWMLKDGIIPEFVSFLIR 263  
 QY 266 KMKRQRPAAVQTEEQRYFLHYHTVAQMF---CSTLQNASPHYQNIKENCAP 312  
 DB 264 EMRTQPSLVQTEQYELVYNVAVLELFKQMDVIRDKHSGTSGAKHCIP 313  
 RESULT 12  
 ABB57374  
 ID ABB57374 standard; protein; 773 AA.  
 XX ABB57374;  
 AC  
 XX 07-MAR-2002 (first entry)  
 DT Mouse ischaemic condition related protein sequence SEQ ID NO:1064.  
 XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.  
 XX Mus musculus.  
 OS  
 XX WO200188189-A2.  
 FN 22-NOV-2001.  
 PD 18-MAY-2001; 2001WO-JP004192.  
 PF 18-MAY-2000; 2000JP-00145977.  
 PR







Wed Dec 8 09:08:32 2004

Search completed: December 7, 2004, 09:49:35  
Job time : 76 secs

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XX WO2003068984-A2.
PN
XX
XX
XX 21-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-EP001446.
XX
XX 13-FEB-2002; 2002US-0356810P.
PR
XX 12-FEB-2003; 2003US-00366547.
PR
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PA
XX (CEPT-) CEPTIR INC.
PA
XX
XX Toraks NK, Tzu-Ching M, Cool DE;
XX
XX WPI; 2003-712572/67.
XX
XX N-PSDB; ADL16221.
XX
XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 71; 238pp; English.
XX
XX The invention relates to a method for identifying a protein tyrosine
XX phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX subjecting a sample, including a cell that contains at least one PTP, to
XX conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX anaerobically, in presence of a sulphydryl-reactive agent (II) that
XX irreversibly modifies the thiol group of an invariant Cys in the active
XX site of PTP; and (iii) determining, under reducing conditions, the level
XX of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX dephosphorylation indicates that an active PTP is present. No details
XX of tests for these activities are given. The method is used to identify
XX reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX are involved. These agents are potentially useful, in human or veterinary
XX medicine, for treating abnormal cell proliferation or growth (cancer);
XX guest vs. host disease; autoimmune diseases; allergy or other
XX immunosuppressed states; metabolic disorders and cell-cycle
XX abnormalities. This sequence represents one of the PTP enzyme of the
XX invention.
XX
XX Sequence 780 AA;
SQ
Query Match 29.2%; Score 709; DB 7; Length 780;
Best Local Similarity 40.7%; Pred. No. 5.5e-56;
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
QY 9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYK 63
DB 8 RKFIQRVQAMKSPDHNGEDN--PARDFWLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65
QY 64 DVLVDQTRVILSLLOEGHSDYINGNFIKRGVDSGLAYIATQGPILPHITLDFWRLWFEFG 123
DB 66 DILPDPHSRVLTKLTPTSQSDSDYINANFIKGYGFKAYVATQGPLANTVIDFWRMIWEYN 125
QY 124 VKVILMACREIENGKRCERYK-AQEORPLQTGLFCITLKEKWLNEIDMLRLTKLVTFQK 182
DB 126 VVILVACREPEMGKCKERYWFLYGEDFITFAFKIS-CEDEQARTDYFIRTLILLFQON 184
QY 183 ESRVYQLQYMSWPDGRGVSPDHHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGLCTV 242
DB 185 ESRRLYQFHYVNWPDHDPVSSFDISLDMISLMRYQHEHEDVPICIHCSAGCGRTGAICAI 244
QY 243 DYVROLILLTQMTPDFSLFDVVILKNRKQRPAAVOTEEQRYLYHTVACMFCSTLQNASPH 302
DB 245 DYTWNLLKAGKIPFEBFNFLQENRTQRHSAVQTPKEQYELVHRAIQALFEKQLQLYEIH 304
QY 303 YQNIKENCAPLYDDALFLRTPOALLAI-----PRPPGGVLRISVPG 344
DB 305 -----GAQKIADGVNEINTENMISSIEPEKQDSPPKPPR--TRSCLVEG 347
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:18 ; Search time 39 Seconds  
(without alignments)  
778.811 Million cell updates/sec

Title: US-10-087-993A-36  
Perfect score: 2424  
Sequence: 1 MRSLSARSFLERLEARGG.....NLRIKRPKGRDPPAEWTRV 458

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778.5	73.4	453	3	US-08-821-278A-2
2	1754.5	72.4	453	3	US-08-951-260A-7
3	1754.5	72.4	453	4	US-08-430-626A-7
4	1754.5	72.4	453	4	US-10-243-687-7
5	830	34.2	155	3	US-08-821-278A-17
6	755.5	31.2	802	3	US-09-081-345-18
7	727.5	30.0	807	3	US-09-081-345-2
8	715.5	29.5	278	3	US-08-821-278A-18
9	695	28.7	272	3	US-08-821-278A-19
10	665	27.4	253	2	US-08-685-992-20
11	665	27.4	253	2	US-08-144-925-20
12	493.5	20.4	255	2	US-08-685-992-16
13	493.5	20.4	255	2	US-09-144-925-16
14	474	19.6	1711	2	US-08-342-930-2
15	467	19.3	595	1	US-08-202-389-6
16	465	19.2	631	1	US-08-202-389-8
17	463.5	19.1	277	2	US-08-685-992-22
18	463.5	19.1	277	2	US-08-144-925-22
19	463.5	19.1	513	1	US-08-202-389-2
20	463	19.1	843	4	US-09-417-197-117
21	463	19.1	853	4	US-09-417-197-119
22	461	19.0	593	1	US-08-018-129-5
23	461	19.0	593	2	US-08-448-250-5
24	461	19.0	593	4	US-08-282-257-5
25	456	18.8	263	2	US-08-685-992-13
26	456	18.8	266	2	US-09-144-925-13
27	454	18.7	266	2	US-08-685-992-12

28	454	18.7	266	2	US-09-144-925-12	Sequence 12, Appl
29	453	18.7	593	1	US-08-202-389-12	Sequence 12, Appl
30	448.5	18.5	232	2	US-08-446-345-38	Sequence 38, Appl
31	448	18.5	913	4	US-08-848-294-2	Sequence 2, Appl
32	441.5	18.2	242	2	US-08-685-992-21	Sequence 21, Appl
33	441.5	18.2	242	2	US-08-144-925-21	Sequence 21, Appl
34	435	17.9	1337	3	US-08-854-585-2	Sequence 2, Appl
35	435	17.9	1337	4	US-09-447-533-2	Sequence 2, Appl
36	435	17.9	1337	5	PCT-US95-05512-2	Sequence 7, Appl
37	433	17.9	244	4	US-08-848-294-7	Sequence 16, Appl
38	429.5	17.7	278	1	US-08-201-697-16	Sequence 37, Appl
39	429	17.7	231	2	US-08-446-345-37	Sequence 57745, A
40	427	17.6	566	4	US-09-270-767-57745	Sequence 4450, A
41	427	17.6	823	4	US-08-270-767-42450	Sequence 1, Appl
42	426.5	17.6	802	1	US-08-015-985-1	Sequence 1, Appl
43	426.5	17.6	802	4	US-08-280-597-1	Sequence 7, Appl
44	426	17.6	258	2	US-08-685-992-19	Sequence 19, Appl
45	426	17.6	258	2	US-09-144-925-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-08-821-278A-2  
; Sequence 2, Application US/08821278A  
; Patent No. 6238902  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: Protein Tyrosine Phosphatases  
; FILE REFERENCE: P1010R1  
; CURRENT APPLICATION NUMBER: US/08/821,278A  
; CURRENT FILING DATE: 1997-03-20  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO 2  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-08-821-278A-2

Query Match	73.4%	Score	1778.5	DB 3	Length	453			
Best Local Similarity	74.9%	Pred. No.	9.2e-154						
Matches	344	Conservative	32	Mismatches	76	Indels	7	Gaps	2
QY	1	MRSLSARSFLERLEARGGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKN	60						
Db	1	MSRHTDLVRSFLEQLEARDYREGAIFVREFSDIKARSVANKSEGVCSFKAGSRLGNTWKN	60						
QY	61	RYKDVLPYDQTRVILSLQEEGHSDYINGNFIRGVDGSLAVIATQGPLHTLLDFWRLVW	120						
Db	61	RYKDVVADTEIVILSLQEEGHGNYINANFIRGIDGSOAVIATQGPLHTLLDFWRLVW	120						
QY	121	EFQVKVILMACREINGRKRERYWAQOEPIQTGLFCITLIKRWLNEDIMRLTKVTF	180						
Db	121	EFQVKVILMACOETENGRRKERYWAQOEPLKAGFCITLTKETLLNADITLRTQVTF	180						
QY	181	QKESRVYQLOYSWPDGVRSSPDHMLAWVEEARLQSGPEPLCVHCSAGCGRTGVLC	240						
Db	181	QKFRSVHQLQYMSWDHGVPSSSHILTWVEARCLQGLGPGPLCVHCSAGCGRTGVLC	240						
QY	241	TVDYVRQLLLTQWIPDFSLFDVILMKRKORPAAYOTEQVRFVHTVQAQPCSTLQNAS	300						
Db	241	AVDYVRQLLLTQTIPNFSLFQVLEMRKORPAAYOTEQVRFVHTVQAQFSLRTQDTS	300						
QY	301	PHYQNKENCALFYDDALFLRTPQALLAIIPRPGGVLRISIVPGSPGHAMADTYAEOKR	360						
Db	301	PHYQNKENCALPICAEAFSLRTSSALPATSRPPGGVLRISIVPAPPTUPMADTYAVQKR	360						
QY	361	GAPAGAGSGTGTGTGARSAAEEAPLYSKVTTPRAQRPQAHADARGTLP-GRVPADQSPA	419						
Db	361	GASAGTGPGRAPTST-----DTPIYSQVAPRAQRPVAHTEDAQGTTLRRVVPADQSS	414						

QY 420 GSGAYEDVAGGATGGLGNLRIGRPGKPRDPPAEWTRV 458  
 DB 415 GPDAYEEDVAGGATGGLGNLRIGRPGKPRDPPAEWTRV 453

RESULT 2  
 US-08-951-260A-7  
 ; Sequence 7, Application US/08951260A  
 ; Patent No. 6004791  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aoki, Nachito  
 ; APPLICANT: Ullrich, Axel  
 ; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
 ; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSEQ for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/951,260A  
 ; FILING DATE: October 16, 1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/030,860  
 ; FILING DATE: NO. 6004791ember 13, 1996  
 ; APPLICATION NUMBER: PCT/1897/00946  
 ; FILING DATE: June 17, 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 227/004  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 453 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-951-260A-7

Query Match 72.4%; Score 1754.5; DB 3; Length 453;  
 Best Local Similarity 74.5%; Pred. No. 1.4e-151;  
 Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

QY 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIQACSAWKADGVCSTVAGSRPENVRKN 60  
 DB 1 MSRQSLVRSFLERLEARGREGAVLAGEFSDIQACSAWKADGVCSTVAGSRPENVRKN 60  
 QY 61 RYKDVLPYDTRVLSLQEGHSDYNGNFRGVDGSLAYIATOGPLPHLLDFRWLW 120  
 DB 61 RYKDVVPYDTRVLSLQEGHSDYNGNFRGVDGSLAYIATOGPLPHLLDFRWLW 120  
 QY 121 EFGKVLWMAEIEGRKCRERYNAQCEPLQGLFCITLKEKWLNEIMRLTKVTF 180  
 DB 121 EFGKVLWMAEIEGRKCRERYNAQCEPLQGLFCITLKEKWLNEIMRLTKVTF 180  
 QY 181 QKESRSVYQLQYMSWPDHGVPSDDHILMTWBEARCLQGLPGPLCVHCSAGCGRTGVLC 240

DB 181 QKESRPVHQLQYMSWPDHGVPSDDHILMTWBEARCLQGLPGPLCVHCSAGCGRTGVLC 240  
 QY 241 TVDYVQLLLTQMIIPDPFSLFDVVLKORQORPAAVOTEEQYRFLYHTVAQMFCSLQNAS 300  
 DB 241 ADVYVQLLLTQMIIPDPFSLFDVVLKORQORPAAVOTEEQYRFLYHTVAQMFCSLQNAS 300  
 QY 301 PHYONIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRISIVPGSPGHAMADTYAEQKR 360  
 DB 301 PHYONIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRISIVPGSPGHAMADTYAEQKR 360  
 QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTTPRQRPGAHAEDARGTLP-GRVPADQSPA 419  
 DB 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTTPRQRPGAHAEDARGTLP-GRVPADQSPA 419  
 QY 420 GSGAYEDVAGGATGGLGNLRIGRPGKPRDPPAEWTRV 458  
 DB 415 GPDAYEEDVAGGATGGLGNLRIGRPGKPRDPPAEWTRV 453

RESULT 3  
 US-09-430-626A-7  
 ; Sequence 7, Application US/09430626A  
 ; Patent No. 6482605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aoki, Nachito  
 ; APPLICANT: Ullrich, Axel  
 ; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
 ; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSEQ for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/430,626A  
 ; FILING DATE: 29-Oct-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/951,260  
 ; FILING DATE: October 16, 1997  
 ; APPLICATION NUMBER: 60/030,860  
 ; FILING DATE: NO. 6482605ember 13, 1996  
 ; APPLICATION NUMBER: PCT/1897/00946  
 ; FILING DATE: June 17, 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 227/004  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 453 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 ; US-09-430-626A-7

Query Match 72.4%; Score 1754.5; DB 4; Length 453;



Query Match 34.2%; Score 830; DB 3; Length 155;

Best Local Similarity 100.0%; Pred. No. 6.7e-68;

Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ARGREGAVLAGEFSDIQCSAAWKADGVCSTVAGSRPENVKRYKDVLPYDQTRVLS 76

DB 1 ARGREGAVLAGEFSDIQCSAAWKADGVCSTVAGSRPENVKRYKDVLPYDQTRVLS 60

QY 77 LQEEGSHSYINGNFIRGVDGSLAVIATQGPLPHTLLDFWRLVWFGVKVILMACREIEN 136

DB 61 LQEEGSHSYINGNFIRGVDGSLAVIATQGPLPHTLLDFWRLVWFGVKVILMACREIEN 120

QY 137 GKRCERYWAQOEPLQTLKWLKWLNEDI 171

DB 121 GKRCERYWAQOEPLQTLKWLKWLNEDI 155

# RESULT 6

US-09-081-345-18

; Sequence 18, Application US/09081345

; Patent No. 6228641

; GENERAL INFORMATION:

; APPLICANT: Bahija Jallal

; APPLICANT: Gregory D. Plowman

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: PTP04 RELATED DISORDERS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/081,345

; FILING DATE: Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/047,222

; FILING DATE: May 20, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/253

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 802 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-081-345-18

Query Match

Best Local Similarity 31.2%; Score 755.5; DB 3; Length 802;

Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 AGEFSDIQCSAAWKADGVCSTVAGSRPENVKRYKDVLPYDQTRVLSLLQEGHSDY 86

DB 25 ASEFLKLRQSKYKADKIYPTVAQRPNKIKKRYKDILPSHLSVLSLTSDESDSY 84

QY 87 INGNFIRGVDGSLAVIATQGPLPHTLLDFWRLVWFGVKVILMACREIENGKRCERYWA 146

DB 85 INASFIKGVYGPAYATQGPLSTLLDFWRLVWFGVKVILMACREIENGKRCERYWA 144

QY 147 QEOE-PLQTLKWLKWLNEDIIMRLTKVTFOKESRVVQLQMSWPDGVPSSPD 205

DB 145 EPQETOLQGFPSISCEAEK-KKSDYKIKTLKAKFNNEIRIIVQHYKWPDPDVPSSD 203

QY 206 HMLAMVEARRIQSGSPBLCVHCSAGCGRTGVLCTVDVYVROLLTQMTPPDPSLFDVVL 265

DB 204 PILQLIWMRCYQEDDCVPICHCSAGCGRTGVCIVCAVDYTWMLLDGIIIPKNSFVNLIQ 263

QY 266 KMEKQRPAAVQTEQYRFLYHTVAOMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPOA 325

DB 264 EMTRQPSLVQTEQYELVISAVLEP-----KHMVDVSDNHLG-----REIQA 308

QY 326 LLAIAPRPGGVLSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTG 377

DB 309 QCSIEP-----QSLTVEADSCPLDLPKNAMRDVKTTHQSKQGAESAETGGSLGLRTS 362

QY 378 ARSAEE 383

DB 363 TMAEE 368

# RESULT 7

US-09-081-345-2

; Sequence 2, Application US/09081345

; Patent No. 6228641

; GENERAL INFORMATION:

; APPLICANT: Bahija Jallal

; APPLICANT: Gregory D. Plowman

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: PTP04 RELATED DISORDERS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/081,345

; FILING DATE: Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/047,222

; FILING DATE: May 20, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/253

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 807 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-081-345-2



Query Match 30.0%; Score 727.5; DB 3; Length 807;  
Best Local Similarity 46.9%; Pred. No. 1.6e-57;  
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;  
  
QY 27 AGFSDIQACSAAWKADGVCSTVAGSRPENVRKRYKDVLPDQTRVILSLLOEGHSDY 86  
DB 25 ANEFLKRGSTKYKADKYPTTVAEKPKIKKRYKIDLPYDSRVLSLTSDESDSY 84  
QY 87 INGNFIRGVDSGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 146  
DB 85 INANFIKGVGPAYATQGPLSTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 144  
QY 147 QEQE-PLQTGLFCITLKEKWLNEIDMLRTLKVTFOKESRVYQLYQMSWPDGVPSSPD 205  
DB 145 EPGEMQLFEGFVSCEAEK-RKSDVIIRTLKVKFNSETRTIYQPHYKNWPDHVPSSID 203  
QY 206 HMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPDPSLFDVVL 265  
DB 204 PILELWDMRCYQEDDSVP:CIHCSAGCGRTGVCICAIDYTWMLLKDGIIIPNFSVFLIR 263  
QY 266 KMKQKORPAAVQTEQRYFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312  
DB 264 EMRTQPSLVQTEQRYELVYNVAVLELFRKQMDVIRDKHSGTESQAKHCIP 313  
  
RESULT 8  
US-08-821-278A-18  
; Sequence 18, Application US/08821278A  
; Patent No. 6238902  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: Protein Tyrosine Phosphatases  
; FILE REFERENCE: P1010R1  
; CURRENT APPLICATION NUMBER: US/08/821,278A  
; CURRENT FILING DATE: 1997-03-20  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO 18  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-08-821-278A-18

Query Match 29.5%; Score 715.5; DB 3; Length 278;  
Best Local Similarity 48.9%; Pred. No. 4.3e-57;  
Matches 139; Conservative 45; Mismatches 91; Indels 9; Gaps 3;  
  
QY 27 AGFSDIQACSAAWKADGVCSTVAGSRPENVRKRYKDVLPDQTRVILSLLOEGHSDY 86  
DB 2 ASEFLKRGSTKYKADKYPTTVAQPKIKKRYKIDLPYDHSVLSSLTSDSDSY 61  
QY 87 INGNFIRGVDSGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 146  
DB 62 INASFIKGVGPAYATQGPLSTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 121  
QY 147 QEQE-PLQTGLFCITLKEKWLNEIDMLRTLKVTFOKESRVYQLYQMSWPDGVPSSPD 205  
DB 122 EPGETQLQFGFVSCEAEK-KKSDYKIRTLKAFNNETRIIYQPHYKNWPDHVPSSID 180  
QY 206 HMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPDPSLFDVVL 265  
DB 181 PILELWDMRCYQEDDSVP:CIHCSAGCGRTGVCICAIDYTWMLLKDGIIIPNFSVFLIR 240  
QY 266 KMKQKORPAAVQTEQRYFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 309  
DB 241 EMRTQPSLVQTEQRYELVYNVAVLELFRKQMDVIRDKHSGTESQAKHCIP 277

RESULT 9  
US-08-821-278A-19  
; Sequence 19, Application US/08821278A  
; Patent No. 6238902  
; GENERAL INFORMATION:

APPLICANT: Cheng, Jill  
APPLICANT: Lasky, Laurence A.  
TITLE OF INVENTION: Protein Tyrosine Phosphatases  
FILE REFERENCE: P1010R1  
CURRENT APPLICATION NUMBER: US/08/821,278A  
CURRENT FILING DATE: 1997-03-20  
NUMBER OF SEQ ID NOS: 23  
SEQ ID NO 19  
LENGTH: 272  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-08-821-278A-19  
  
Query Match 28.7%; Score 695; DB 3; Length 272;  
Best Local Similarity 47.1%; Pred. No. 3.1e-55;  
Matches 128; Conservative 55; Mismatches 87; Indels 2; Gaps 2;  
  
QY 27 AGFSDIQACSAAWKADGVCSTVAGSRPENVRKRYKDVLPDQTRVILSLLOEGHSDY 86  
DB 2 ARDFWELRLSTKYKTEKIYPTATGEKEENVKRYKIDLPFDHRSVKLTILKTPSQSDSY 61  
QY 87 INGNFIRGVDSGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 145  
DB 62 INANFIKGVGPAYATQGPLSTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 121  
QY 146 AQEQEPLQTGLFCITLKEKWLNEIDMLRTLKVTFOKESRVYQLYQMSWPDGVPSSPD 205  
DB 122 LYGEDPITTFAPFKIS-CEDEQARTDYFIRTLLEFQNESRRLYQPHYKNWPDHVPSSFD 180  
QY 206 HMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPDPSLFDVVL 265  
DB 181 STLDWISLMRKYQEHEDVPICIHCSAGCGRTGCAIDYTWMLLKAGKIPPEFNVFLIQ 240  
QY 266 KMKQKORPAAVQTEQRYFLYHTVAQMFCSLTQ 297  
DB 241 EMRTQPSLVQTEQRYELVYNVAVLELFRKQMDVIRDKHSGTESQAKHCIP 272

RESULT 10  
US-08-685-992-20  
; Sequence 20, Application US/08685992  
; Patent No. 5912138  
; GENERAL INFORMATION:  
; APPLICANT: Tonks, Nicholas  
; APPLICANT: Flint, Andrew J.  
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
; TITLE OF INVENTION: TYROSINE PHOSPHATASES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,992  
; FILING DATE: 25-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL96-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-685-992-20

Query Match 27.4%; Score 665; DB 2; Length 253;

Best Local Similarity 49.4%; Pred. No. 1.5e-52;

Matches 126; Conservative 44; Mismatches 73; Indels 12; Gaps 3;

QY 48 TVAGSRPENVRKRYKDVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAYIATQGP 107

Db 4 TATGEKEENVKRYKDIPLPDHRSVKLTLPKTPSQSDYINANFVGVGPKAYVATQGP 63

QY 108 LPHLLDFWRLVWFGVKVILMACREIENGRKRCERYW-AQOEPLQTLGFCITLKEKW 166

Db 64 LANTVIDFWMVWYVNVIIVMACREFENGKRCERYWPLYGDDPTTAPFKISC----- 118

QY 167 LNEIDIMLRT-----LKVTFOKESRSVYQYMSWPDRCVPSDPDHMLAMVEEARLQSGSP 222

Db 119 --EDEQARTDYFILLFQNESRRLYQFHYVNPDPHDVPSSFDLSILMSLMKRYQEHED 176

QY 223 EPLCVHCSAGCGRTGVLCTVDYVROLILLTQMIPDPFSLFDVVLKMKRKPAAVQTEQYR 282

Db 177 VPICHCISAGCGRTGAICAIDYTNLLKAGKIPESFNVLQIEMRTQHSVAQTKEQYE 236

QY 283 FLYHTVAQMFCSTLQ 297

Db 237 LVHRAIAQLFEKQLQ 251

RESULT 11

US-09-144-925-20

Sequence 20, Application US/09144925

Patent No. 5951979

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02421-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,925

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,992

FILING DATE: July 25, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03Z

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-144-925-20

Query Match 27.4%; Score 665; DB 2; Length 253;

Best Local Similarity 49.4%; Pred. No. 1.5e-52;

Matches 126; Conservative 44; Mismatches 73; Indels 12; Gaps 3;

QY 48 TVAGSRPENVRKRYKDVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAYIATQGP 107

Db 4 TATGEKEENVKRYKDIPLPDHRSVKLTLPKTPSQSDYINANFVGVGPKAYVATQGP 63

QY 108 LPHLLDFWRLVWFGVKVILMACREIENGRKRCERYW-AQOEPLQTLGFCITLKEKW 166

Db 64 LANTVIDFWMVWYVNVIIVMACREFENGKRCERYWPLYGDDPTTAPFKISC----- 118

QY 167 LNEIDIMLRT-----LKVTFOKESRSVYQYMSWPDRCVPSDPDHMLAMVEEARLQSGSP 222

Db 119 --EDEQARTDYFILLFQNESRRLYQFHYVNPDPHDVPSSFDLSILMSLMKRYQEHED 176

QY 223 EPLCVHCSAGCGRTGVLCTVDYVROLILLTQMIPDPFSLFDVVLKMKRKPAAVQTEQYR 282

Db 177 VPICHCISAGCGRTGAICAIDYTNLLKAGKIPESFNVLQIEMRTQHSVAQTKEQYE 236

QY 283 FLYHTVAQMFCSTLQ 297

Db 237 LVHRAIAQLFEKQLQ 251

RESULT 12

US-08-685-992-16

Sequence 16, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992

FILING DATE: 25-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-06-685-992-16

Query Match
Best Local Similarity 20.4%; Score 493.5; DB 2; Length 255;
Matches 115; Conservative 36; Mismatches 94; Indels 19; Gaps 7;

QY 47 STVAGSRPNVRKRYKDVLPYDQTRVILSLLOEGHSDYINGNFRGVDSGLAYIATQG 106
Db 3 SOMVASSENNAKRYRNVLFDWSRVLPKPIHEEFGSDYINAFMPLGWSPOEFATQG 62
QY 107 PLPHTLDFWRLVWFGVKVILMACREIENGKRCERYWAOEPLQTGLFCITLKEKW 166
Db 63 PLPQTGVGFWRVWEOQSHLTMLTNCMEAGRVKCEHYWPLDSQPTHGHLRVTLVGEV 122
QY 167 LNEDEMLATIKVTFOKESRSVYQYQMSWPDGRGVSPSPDHMLAMVEEAR- 221
Db 63 PLPQTGVGFWRVWEOQSHLTMLTNCMEAGRVKCEHYWPLDSQPTHGHLRVTLVGEV 122
QY 167 LNEDEMLATIKVTFOKESRSVYQYQMSWPDGRGVSPSPDHMLAMVEEAR- 221
Db 123 MENWTVLLQLQVEEQK-TLSVRQHYQAWPDHGVSPSPDTHLAFWRLRQWLDQTMGGP 181
QY 222 PEPLCHVCSAGCGRTGVLCTVD-YVRQLLLTQMIPDPDFSLFDVVLKMRKORPAAVQTEEQ 280
Db 182 P---IVHCSAGVGRGTGLIALDVLRLQSEGLIGP-----FSFVKMRRESPLMVQTEAQ 234
QY 281 YRFLYHTVAQMFCTSLQNASPHYQ 304
Db 235 YVFLH-----QCICGS-SNSQPRPQ 253

RESULT 14
US-08-342-930-2
; Sequence 2, Application US/08342930
; Patent No. 5821084
; GENERAL INFORMATION:
; APPLICANT: OLMSTED, ELIZABETH A.
; APPLICANT: MAURO, LAURA J.
; APPLICANT: DAVIS, ALAN R.
; APPLICANT: DIXON, JACK E.
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,930
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20975.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1711 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-342-930-2
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; LENGTH: 255 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-06-685-992-16

Query Match
Best Local Similarity 20.4%; Score 493.5; DB 2; Length 255;
Matches 115; Conservative 36; Mismatches 94; Indels 19; Gaps 7;

QY 47 STVAGSRPNVRKRYKDVLPYDQTRVILSLLOEGHSDYINGNFRGVDSGLAYIATQG 106
Db 3 SOMVASSENNAKRYRNVLFDWSRVLPKPIHEEFGSDYINAFMPLGWSPOEFATQG 62
QY 107 PLPHTLDFWRLVWFGVKVILMACREIENGKRCERYWAOEPLQTGLFCITLKEKW 166
Db 63 PLPQTGVGFWRVWEOQSHLTMLTNCMEAGRVKCEHYWPLDSQPTHGHLRVTLVGEV 122
QY 167 LNEDEMLATIKVTFOKESRSVYQYQMSWPDGRGVSPSPDHMLAMVEEAR- 221
Db 63 PLPQTGVGFWRVWEOQSHLTMLTNCMEAGRVKCEHYWPLDSQPTHGHLRVTLVGEV 122
QY 167 LNEDEMLATIKVTFOKESRSVYQYQMSWPDGRGVSPSPDHMLAMVEEAR- 221
Db 123 MENWTVLLQLQVEEQK-TLSVRQHYQAWPDHGVSPSPDTHLAFWRLRQWLDQTMGGP 181
QY 222 PEPLCHVCSAGCGRTGVLCTVD-YVRQLLLTQMIPDPDFSLFDVVLKMRKORPAAVQTEEQ 280
Db 182 P---IVHCSAGVGRGTGLIALDVLRLQSEGLIGP-----FSFVKMRRESPLMVQTEAQ 234
QY 281 YRFLYHTVAQMFCTSLQNASPHYQ 304
Db 235 YVFLH-----QCICGS-SNSQPRPQ 253

RESULT 13
US-09-144-925-16
; Sequence 16, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,992
; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
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Query Match 19.6%; Score 474; DB 2; Length 1711;  
Best Local Similarity 39.9%; Pred. No. 6.2e-34;  
Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;  
QY 10 SFLELEARGREGAVLAGEFSDIQACSAAMKADGVCSTVAGSRPENVRKRYKDVLPYD 69  
Db 1134 SFRQSEAKSAHAQTFQEFELKEVGKQ-----PRLEAEHPDNIKRYPHVLPYD 1187  
QY 70 QTEVTLSSLOEGHSDYINGNIRGVDSGLAVIATQGPLPHTLLDFWRLVWFEFGVKVILM 129  
Db 1188 HSRVRLTQPGFSDYINANIPGVSHQTEIATQGPLKLTLEDFWRLVWFEQVHVILM 1247  
QY 130 ACREIENGKRCERYWAQOEPLQGLFCITILKE-----KWLNEDIMLRTLKVTFOKESR 185  
Db 1248 LTVGMENGRVLCHEHYWPANSTPTVTHGHTIHLAEPEDEWTRREFQLQ--HGTEQKQ-R 1304  
QY 186 SVYQLOYSWPDGRGVPSSPDHMLMV-----EARRLOGSGPEPLCVHCSAGCGRTGVLC 241  
Db 1305 RVKQLQFTTPDHSVPEAPSSLLAFVELVQEQVQATQCKG--PILVHCSAGVGRTGT--- 1359  
QY 242 VDVROLLLTOMIPPD--EFLFDVVLKMRKORPAAVQTEEQRYFLY 285  
Db 1360 --FVALLRLRLQEEKQVADVENTVYILRLHRLPMLQIQLSQYIFLH 1403

RESULT 15  
US-08-202-389-6  
Sequence 6, Application US/08202389  
Patent No. 5536636  
GENERAL INFORMATION:  
APPLICANT: Freeman Jr., Robert M.  
APPLICANT: Plutzky, Jorge  
APPLICANT: Neel, Benjamin G.  
APPLICANT: Rosenberg, Robert D.  
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE  
SEQUENCE INFORMATION: PHOSPHATASES HAVING SH2 DOMAINS  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,389  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,926  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/829,141  
FILING DATE: 31-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/721,112  
FILING DATE: 26-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BI92-05MA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-202-389-6  
Query Match 19.3%; Score 467; DB 1; Length 595;  
Best Local Similarity 32.9%; Pred. No. 6e-34;  
Matches 112; Conservative 57; Mismatches 109; Indels 62; Gaps 10;  
QY 22 EGAVLAG---EFSDIQACSAAMKADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILSLL 78  
Db 237 EDTAKAGFWEEFESLQ-----KQEVKVLHQLRLEGORPENKGRYKNILPFDHSRVIL--- 289  
QY 79 QEEGH-----SDYINGNIRGV-----DGLAYIATQGPLPHTLLDFWRLVWFEFGVKVI 127  
Db 290 --QGRDSNIPGSDYINANIPKQQLGPDENAKTYIASQGCLEATVNDPQMAQENSRVI 347  
QY 128 LMACREIENGKRCERYWAQOEPLQGLFCITILKEKWLNEDIMLRTLKVTFOKES--- 184  
Db 348 VMTREVEKGRNKCVPYWEVGMQRAYGYSVINVEGHTTE-YKLRILQVSPDLNGDLI 406  
QY 185 RSVYQLOYSWPDGRGVPSSPDHMLMV-----EARRLOGSGPE--PLCVHCSAGCGRTGVLC 242  
Db 407 REIWHYQYLSWPDHGVSEPGVLSFLDQINQROESLPHAGPIIVHCSAGIGRTGTIIVI 466  
QY 243 DYVRQLLLTOMIPPDSEFLFDVVLKMRKORPAAVQTEEQRYFLYHTVQMFCS--- 295  
Db 467 DMLMENISTKGLDCDIDIOKTQMVRQSRGMVQTEAQYKFIYVAIAQFIETIKKLEVL 526  
QY 296 -----LQNA-----SPHYQNIKEN 309  
Db 527 QSQKQGESEYGNITYPPAMKNAHAKASRTSSKHEDVYEN 566

Search completed: December 7, 2004, 09:54:25  
Job time : 41 secs

14	705.5	29.1	382	14	US-10-366-547-77	Sequence 77, Appl
15	703	29.0	14	US-10-366-547-75	Sequence 75, Appl	
16	665	27.4	312	9	US-09-788-626-21	Sequence 21, Appl
17	523	21.6	235	15	US-10-087-684-94	Sequence 94, Appl
18	523	21.6	235	15	US-10-218-779-94	Sequence 94, Appl
19	523	21.6	235	15	US-10-072-012-819	Sequence 819, Appl
20	521.5	21.5	263	15	US-10-087-684-93	Sequence 93, Appl
21	521.5	21.5	263	15	US-10-218-779-93	Sequence 93, Appl
22	496.5	20.5	264	14	US-10-245-539-6	Sequence 6, Appl
23	493.5	20.4	313	9	US-09-788-626-17	Sequence 17, Appl
24	491.5	20.3	1093	14	US-10-245-539-4	Sequence 4, Appl
25	491.5	20.3	1118	14	US-10-245-539-2	Sequence 2, Appl
26	491.5	20.3	1118	14	US-10-245-539-8	Sequence 8, Appl
27	482.5	19.9	613	14	US-10-366-547-97	Sequence 97, Appl
28	463.5	19.1	341	9	US-09-788-626-23	Sequence 23, Appl
29	463	19.1	595	9	US-09-920-021A-1	Sequence 1, Appl
30	463	19.1	595	14	US-10-366-547-87	Sequence 87, Appl
31	463	19.1	595	14	US-10-366-547-91	Sequence 91, Appl
32	463	19.1	597	14	US-10-366-547-89	Sequence 89, Appl
33	463	19.1	621	15	US-10-264-049-3086	Sequence 3086, Ap
34	463	19.1	843	14	US-10-072-036-117	Sequence 117, App
35	463	19.1	843	14	US-10-072-036-119	Sequence 119, App
36	458	18.9	593	14	US-10-262-552-2	Sequence 2, Appl
37	458	18.9	593	14	US-10-366-547-26	Sequence 26, Appl
38	458	18.9	593	16	US-10-703-210-2	Sequence 2, Appl
39	456	18.8	322	9	US-09-788-626-14	Sequence 14, Appl
40	454	18.7	325	9	US-09-788-626-13	Sequence 13, Appl
41	453	18.7	593	9	US-09-920-021A-3	Sequence 3, Appl
42	453	18.7	593	14	US-10-366-547-28	Sequence 28, Appl
43	453	18.7	593	14	US-10-366-547-30	Sequence 30, Appl
44	453	18.7	593	14	US-10-366-547-32	Sequence 32, Appl
45	453	18.7	593	15	US-10-444-795B-789	Sequence 789, App

ALIGNMENTS

*Handwritten signature*

RESULT 1  
US-10-087-993-36  
; Sequence 36, Application US/10087993  
; Publication No. US20020169303A1  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich, Axel  
; Aoki, Naohito  
; Kim, Yeong Woong  
; Wang, Hong Yang  
; Chen, Zhengjun  
; Naylor, Oliver  
; Kharitonov, Alexei Igorevich  
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPL, CLK,  
; AND SIRP POLYPEPTIDES AND RELATED  
; PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA: US/10/087,993  
APPLICATION NUMBER: US/10/087,993  
FILING DATE: 05-Mar-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/877,150

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OM protein - protein search, using sw model  
Run on: December 7, 2004, 09:48:18 ; Search time 61 Seconds  
(without alignments)  
2677.715 Million cell updates/sec

Title: US-10-087-993A-36  
Perfect score: 2424  
Sequence: 1 MSRLSDARSFLERLRGGE.....NLRIKPKGRPPPAETWTV 458

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1582225 seqs, 35663895 residues  
Total number of hits satisfying chosen parameters: 1582225

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	Published Applications AA:*
1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2:	/cgn2_6/ptodata/2/pubpaa/PCN_NEW_PUB.pap.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
6:	/cgn2_6/ptodata/2/pubpaa/PCNUS_PUBCOMB.pap.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pap.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pap.*
17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pap.*
18:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2424	100.0	458	13	US-10-087-993-36
2	1754.5	72.4	453	14	US-10-243-687-7
3	1724.5	71.1	448	13	US-10-087-993-32
4	755.5	31.2	802	9	US-09-822-295-18
5	755.5	31.2	802	14	US-10-366-547-95
6	755.5	31.2	802	15	US-10-309-423-5
7	727.5	30.0	807	9	US-09-822-295-2
8	709	29.2	780	14	US-10-366-547-69
9	709	29.2	780	14	US-10-366-547-71
10	708	29.2	692	15	US-10-309-423-4
11	708	29.2	778	16	US-10-322-281-848
12	708	29.2	808	15	US-10-309-423-2
13	706	29.1	773	16	US-10-322-281-845

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; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:

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Query Match 100.0%; Score 2424; DB 13; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6e-189;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRSLSASRFLERLEARGRGAGVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
DB 1 MRSLSASRFLERLEARGRGAGVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
QY 61 RYKDVLPYQTRVILSLQEBGSDYINGNFIRGVDGSLAYIATQGPLHTLLDFWRLVW 120
DB 61 RYKDVLPYQTRVILSLQEBGSDYINGNFIRGVDGSLAYIATQGPLHTLLDFWRLVW 120
QY 121 EFGVKVILMACRIENGRKRCRYWAQOEPLQTGLFCITLTIKEKWLNEIMRLTKVTF 180
DB 121 EFGVKVILMACRIENGRKRCRYWAQOEPLQTGLFCITLTIKEKWLNEIMRLTKVTF 180
QY 181 QKESRSVYQLQYMSWPDRCVPSPDHMLAMVEARLQSGPEPLCVHCSAGCGRTGVL 240
DB 181 QKESRSVYQLQYMSWPDRCVPSPDHMLAMVEARLQSGPEPLCVHCSAGCGRTGVL 240
QY 241 TVDYVRQLLLTQMIIPDFSLFDVVLKMRKORPAAVQTEQRYFLYHTVAQMFCSLTQNAS 300
DB 241 TVDYVRQLLLTQMIIPDFSLFDVVLKMRKORPAAVQTEQRYFLYHTVAQMFCSLTQNAS 300
QY 301 PHYQNTKENCAPLYDDALFLRTPQALLATPRPGCVILASISVPGSPGHAMADTYAEQKR 360
DB 301 PHYQNTKENCAPLYDDALFLRTPQALLATPRPGCVILASISVPGSPGHAMADTYAEQKR 360
QY 361 GAPAGAGSGTGTGTGARSASEAPLYSKVTTPRAQPGAHADARGTLPGRPVADQSPAG 420
DB 361 GAPAGAGSGTGTGTGARSASEAPLYSKVTTPRAQPGAHADARGTLPGRPVADQSPAG 420
QY 421 SGAYEDVAGAGTGGGLGFLNLRIGRPKGRDPPAEWTRV 458
DB 421 SGAYEDVAGAGTGGGLGFLNLRIGRPKGRDPPAEWTRV 458

```

## RESULT 2

US-10-243-687-7

Sequence 7, Application US/10243687

Publication No. US20030073120A1

GENERAL INFORMATION:

APPLICANT: Aoki, Naohito

Ullrich, Axel

```

; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; AND RELATED PRODUCTS AND METHODS

```

```

; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700

```

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/10/243,687
; FILING DATE: 16-Sep-2002
; CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/430,626A

```

```

; FILING DATE: 29-Oct-1999

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```

; APPLICATION NUMBER: 08/951,260

```

```

; FILING DATE: October 16, 1997

```

```

; APPLICATION NUMBER: 60/030,860

```

```

; FILING DATE: No. US20030073120A1ember 13, 1996

```

```

; APPLICATION NUMBER: PCT/1897/00946

```

```

; FILING DATE: June 17, 1997

```

```

; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Warburg, Richard J.

```

```

; REGISTRATION NUMBER: 32,327

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; REFERENCE/DOCKET NUMBER: 227/004

```

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; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (213) 489-1600

```

```

; TELEFAX: (213) 955-0440

```

```

; TELEX: 67-3510

```

```

; INFORMATION FOR SEQ ID NO: 7:

```

```

; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 453 amino acids

```

```

; TYPE: amino acid

```

```

; STRANDEDNESS: single

```

```

; TOPOLOGY: linear

```

```

; MOLECULE TYPE: peptide

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```

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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US-10-243-687-7

Query Match 72.4%; Score 1754.5; DB 14; Length 453;

Best Local Similarity 74.8%; Pred. No. 1.3e-134;

Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

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QY 1 MRSLSASRFLERLEARGRGAGVLAGFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
DB 1 MRSQSLVRSFLQEQARDHRKGAIIAREFSDIKARSVANKTEGVCS TKAGSQGNSKN 60
QY 61 RYKDVLPYQTRVILSLQEBGSDYINGNFIRGVDGSLAYIATQGPLHTLLDFWRLVW 120
DB 61 RYKDVVPYDETRVILSLQEBGSDYINANFIRGTDGSOAYIATQGPLHTLLDFWRLVW 120
QY 121 EFGVKVILMACRIENGRKRCRYWAQOEPLQTGLFCITLTIKEKWLNEIMRLTKVTF 180
DB 121 EFGVKVILMACQETENGRKRCRYWAQEREPLQAGPFCITLTKETALTSITLRLQVTF 180
QY 181 QKESRSVYQLQYMSWPDRCVPSPDHMLAMVEARLQSGPEPLCVHCSAGCGRTGVL 240
DB 181 QKESRPVHQLQYMSWPDRCVPSDDHILTWBEARCLQGLGPEPLCVHCSAGCGRTGVL 240
QY 241 TVDYVRQLLLTQMIIPDFSLFDVVLKMRKORPAAVQTEQRYFLYHTVAQMFCSLTQNAS 300
DB 241 AVDYVRQLLLTQTIIPNFSLFEVLEMRKORPAAVQTEQRYFLYHTVAQMFCSLTQNAS 300
QY 301 PHYQNTKENCAPLYDDALFLRTPQALLATPRPGCVILASISVPGSPGHAMADTYAEQKR 360

```

Db 301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLSISVPGPPTLPMDATTAVVQKR 360  
QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAORPGAHAEADAGTLP-GRVPADQSPA 419  
Db 361 GA-----SGS-TGPGTRAPNSTDTIYSQVAPRIQRPVSHTEANAQGTALGRVPADENPS 414  
QY 420 GSGAYEDVAGGAQTGGGLGNLRIGRPKGRPRDPPAEWTRV 458  
Db 415 GPDAYEEVTDGAQTGGGLGNLRIGRPKGRPRDPPAEWTRV 453

RESULT 3  
US-10-087-993-32  
; Sequence 32, Application US/10087993  
; Publication No. US20020169303A1  
; GENERAL INFORMATION:  
; APPLICANT: Ullrich, Axel  
; Aoki, Naohito  
; Kim, Yeong Woong  
; Wang, Hong Yang  
; Chen, Zhengjun  
; Naylor, Oliver  
; Khaitonenkov, Alexei Igorevich  
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPI, CLK,  
; AND SIRP POLYPEPTIDES AND RELATED  
; PRODUCTS AND METHODS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/087,993  
; FILING DATE: 05-Mar-2002  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/877,150  
; FILING DATE: June 17, 1997  
; APPLICATION NUMBER: U.S. 60/019,629  
; FILING DATE: June 17, 1996  
; APPLICATION NUMBER: U.S. 60/023,485  
; FILING DATE: August 9, 1996  
; APPLICATION NUMBER: U.S. 60/030,860  
; FILING DATE: No. US20020169303A1ember 13, 1996  
; APPLICATION NUMBER: U.S. 60/034,286  
; FILING DATE: December 19, 1996  
; APPLICATION NUMBER: U.S. 60/030,964  
; FILING DATE: No. US20020169303A1ember 15, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 225/298  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-10-087-993-32  
Query Match 71.1%; Score 1724.5; DB 13; Length 448;  
Best Local Similarity 74.2%; Pred. No. 3.5e-132;  
Matches 337; Conservative 37; Mismatches 73; Indels 7; Gaps 3;  
QY 1 MSRSJDSARSFLERLEARGGREGAVLAGFSDICACSAAMKADGVCSSTVAGSRPENVRKN 60  
Db 1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAMKTEGVCSSTKAGSQGNSKKN 60  
QY 61 RYKDVLPYDQTRVLSLLQEEGSHDYINGNFIRGVDSGLAYIATQGGPLPHTLLDFWRLVW 120  
Db 61 RYKDVVPYDETRVLSLLQEEGSHDYINGNFIRGVDSGLAYIATQGGPLPHTLLDFWRLVW 120  
QY 121 EFGVKVILMACRELENGKRCERYMAQOEPLQGLGSCITLKEKWLNEDEIMLTAKVTF 180  
Db 121 EFGIKVILMACQETENGRRKRCERYMAQOEPLQGLGSCITLKEKWLNEDEIMLTAKVTF 180  
QY 181 QKESRSVYQLQYMSMPDRGVFSSPDHMLAMVVEARLQSGSGPPLCVHCSAGCGRTGVL 240  
Db 181 QKESRPVHQLQYMSMPDRGVFSSPDHMLAMVVEARLQSGSGPPLCVHCSAGCGRTGVL 240  
QY 241 TVDYVROLTLTQMPPDPSLEFNVLMKQKQPPAAVQTEQYRFLYHTVAQMFSTLONAS 300  
Db 241 ADVYVROLTLTQMPPDPSLEFNVLMKQKQPPAAVQTEQYRFLYHTVAQMFSTLONAS 300  
QY 301 PHYQNIKENCAPLYDDALFLTPQALLAIPRPFGGVLSRSISVPGSPGHAMADTYAEEQKR 360  
Db 301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLSISVPGPPTLPMDATTAVVQKR 360  
QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAORPGAHAEADAGTLP-GRVPADQSPA 419  
Db 361 GA-----SGS-TGPGTRAPNSTDTIYSQVAPRIQRPVSHTEANAQGTALGRVPADENPS 414  
QY 420 GSGAYEDVAGGAQTGGGLGNLRIGRPKGRPRDPPA 453  
Db 415 GPDAYEEVTDGAQTGGGLGNLRIGRPKGRPRDPPA 448

RESULT 4  
US-09-822-295-18  
; Sequence 18, Application US/09822295  
; Patent No. US20020119501A1  
; GENERAL INFORMATION:  
; APPLICANT: Bahija Jallal  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/822,295  
; FILING DATE: 02-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/081,345  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:







```

; TITLE OF INVENTION:  PHOSPHATASES
; FILE REFERENCE:  200125.439
; CURRENT APPLICATION NUMBER:  US/10/366,547
; CURRENT FILING DATE:  2003-02-12
; NUMBER OF SEQ ID NOS:  98
; SOFTWARE:  FASTSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH:  780
; TYPE:  PRT
; ORGANISM:  Homo sapiens
; US-10-366-547-71

```

Query Match 29.2%; Score 709; DB 14; Length 780;  
Best Local Similarity 40.7%; Pred. No. 6.9e-49;  
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;

Qy	9	R	F	L	E	R	L	E	A	-----RGREGAVLAGESDIOACSAANKADGVSTVAGSPENVRNR	YK	53																																														
Db	8	R	X	F	I	O	R	V	A	M	K	S	P	D	H	G	E	D	N	-----FADFMRRLRTKYRTKTYPTATGEKEENKVR	YK	65																																				
Qy	64	D	V	L	P	D	T	O	R	V	I	L	S	L	L	Q	E	G	H	S	D	I	N	G	P	I	R	G	V	S	L	A	I	A	T	O	G	P	L	H	L	D	F	M	R	L	V	M	E	E	G		123					
Db	66	D	I	L	P	D	H	S	R	V	K	L	T	K	T	P	S	D	S	I	N	A	N	P	I	K	V	G	P	K	A	V	A	T	O	G	P	L	A	N	T	D	F	M	R	M	I	E	W	E	Y	N		125				
Qy	124	V	K	V	I	L	M	A	C	R	E	I	N	G	R	K	E	R	Y	W	-----AQE	B	P	L	O	T	G	L	F	C	T	L	I	K	E	K	W	L	N	E	D	I	M	L	R	T	K	T	P	O	K		182					
Db	126	V	I	I	W	A	C	R	E	F	M	G	R	K	E	R	Y	G	E	D	I	T	A	P	K	I	S	-----C	E	D	Q	A	R	T	D	Y	F	I	R	L	L	E	F	O	N		184											
Qy	183	E	S	R	V	Y	Q	L	O	G	M	S	W	P	D	R	G	P	S	P	D	H	L	M	A	V	E	A	R	L	O	G	S	G	P	E	P	E	C	V	H	C	S	A	C	G	R	T	G	V	L	T		242				
Db	185	E	S	R	L	Y	Q	F	H	V	N	W	P	D	H	D	P	S	F	S	I	L	M	R	K	Y	Q	E	H	E	R	D	V	P	I	C	H	S	A	C	G	R	T	G	A	I	C	A		244								
Qy	243	D	Y	V	R	O	L	L	T	O	M	T	P	P	S	F	D	V	L	K	M	R	K	O	R	P	A	A	V	O	T	E	S	Q	F	R	L	H	T	V	A	O	M	F	C	S	T	L	Q	N	A	S	P		302			
Db	245	D	Y	T	N	L	L	K	A	G	K	I	P	E	E	F	N	V	N	I	Q	E	M	R	T	O	R	H	S	A	V	O	T	K	Q	Y	E	L	V	H	R	A	I	A	Q	L	F	E	K	O	L	Q	I	Y	E	H		304
Qy	303	Y	Q	N	I	K	E	N	C	A	P	L	Y	D	D	A	L	F	L	E	T	P	O	A	L	I	A	-----P	R	P	P	G	G	V	L	R	S	I	S	V	E	G		344														
Db	305	-----G	A	K	I	A	D	G	V	N	E	I	N	T	E	M	I	S	S	I	P	E	X	Q	D	S	P	P	K	P	P	R	-----T	R	S	C	L	V	E	G		347																

```

RESULT 10
US-10-309-423-4
; Sequence 4, Application US/10309423
; Publication No. US20040006777A1
; GENERAL INFORMATION:
; APPLICANT: HSC Research and Development Limited Partnership
; TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
; FILE REFERENCE: 92906-2
; CURRENT APPLICATION NUMBER: US/10/309,423
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/600,358
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: CA 2,220,853
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-423-4

```

Query Match 29.2%; Score 708; DB 15; Length 692;  
Best Local Similarity 46.7%; Pred. No. 7.1e-49;  
Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;

[illegible]

85	INANFIKGVGYGKAYIATQGLPSTLLD	PWRMIWEYSVLIIVMACMEYENGKKCERYWA	144
Db			
147	QBQE-PLQTGLFCITLIKELWNEDIMLR	LKVTFOKESRVYQLOIYMSWDPDVPSSPD	205
QY			
145	EPGENQLEFGFPVSCEAEK-RKSDYI	IRTLKVKFNSETTIQFHYKNWPDHVDSSID	203
Db			
206	HMLAMVEARLQSGPBPPLCVHCSAG	CGRTGVLCT-VDYVRQLLTQMIPPDFSLFDVV	264
QY			
204	PILELIWDVRCVQEDDSVPICHSAG	CGRTGVCAIVDYVTMLLKXGIIIPENFSVFSLI	263
Db			
265	LKQKQRPAAVCTGEQVRFVHTVAQWF	---CSTLQNASPHYQNIKENCAP	312
QY			
264	RMWRTQSLVCTQOEVLVYNALVLEFK	ROMDVIRDKHSGTSQAQHCIP	314
Db			

```

RESULT 11
US-10-322-281-848
; Sequence 848, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-848

```

Query Match 29.2%; Score 708; DB 16; Length 778;  
Best Local Similarity 40.7%; Pred. No. 8.3e-49;  
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;

Qy	9	RSFLERLEA-----RGGREGAVLAGESDTCQASAAWKADGVCSVTVAGSRPENVRQRYK	63
Db	8	RKFIQRVQAMKSPDHNGEDN--FARDFMRJLRUSTKYRTEKIYPTATGKEBENVKRNYK	65
Qy	64	DVLPYDQTRVILSLLOEBGSHDYINGNPIRGVDSGLAYIATQGPLHTLLDFRLVWFEF	123
Db	66	DILPDHSHSVKLTUKTPSQDSDIYINAFIKGVYGPAYVATQPLANTVDFWRMIWEYN	125
Qy	124	VKVILMACREBENGKRCERYW-AQOBSPQTGLFCITLKEKWLNEIDMLRLKVTFFQK	192
Db	126	VVIIVMACREPFEMGKRCERYWYLGEDPTTFAPFKIS-CEDQOARTDYPFRITLLLEFQN	184
Qy	183	ESRSVYVQLQYMSDPDRGPVSPDPHMLAMVEARLQSGPEPCLVCHSGACGRGTGLVCTV	242
Db	185	ESRRLYQHYVNWPDHDPVSSDFSILDMILSRKYQEHEDVPICIHCSACGRGTGAICAI	244
Qy	243	DYVRQILLITQWIPDPDFSULFDVLVKRRQORPAAVOTEQYRFLVHTVQAMFCSLTQNASPH	302
Db	245	DYTNWLLKAGKIPBEFNFVNIQEMRTQRHSVAVTQEQYELVHRAAQLPEKOLQLYEIH	304
Qy	303	YQNIKENCAPLYDDALFURTPQALLAI-----PRPPGGVLRISIVPG	344
Db	305	-----GACKTADGVNRENTNMVSSSTPEPEKODSPPKPPR--TRSLCVGG	347

RESULT 12  
US-10-309-423-2  
; Sequence 22, Application US/10309423  
; Publication No. US2004000677A1  
; GENERAL INFORMATION:  
; APPLICANT: HSC Research and Development Limited Partnership  
; TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases  
; FILE REFERENCE: 92906-2  
; CURRENT APPLICATION NUMBER: US/10/309.423  
; CURRENT FILING DATE: 2002-12-03

DB Db ESRLYQHYVWPDHDPVSSFDSDILDMISLMRYQEHEDVPICHCSAGCGRTGACAI 244  
QY QY DYVROLLTQMIIPDPDFSLFVVKMKRQBPAAVOTESQYRFLYHTVQMF----- 292  
Db Db DYTWNLLKAGKIPBEFNVFNLIQEMRTORHSAVQTKQYELVHRAIAQLFKQQLQYVEIH 304  
QY QY -----C-----STLQNASPH----- 302  
Db Db GAKTIADGNEITGTMWSSIDSEKQDPPKPPRTRSCLVGEGDAKEEILQPEHPVPP 364  
QY QY -----Y 303  
Db Db LTPSPPSAFTVTVMQDSDRYHPKPVLMHDEQHPADLNRSYDKSADPMGKSEAIHID 424  
QY QY QNIKENCA-----PL-----YDALLFL-----RT--PQALLA----- 328  
Db Db KKLERNLSFEIKVPLQBGPKSFDGNTLLNKGHAIKKSSASSVVDRSKPQELSAGALK 484  
QY QY -----TPRP-----PGVLRSI-----S 341  
Db Db VDDVQNSCADCSAAHSHRAAESSEOSNSHTPPRDCPLDKKKGHVTVSLHGFENATP 544  
QY QY VPGSPGHAMADTY-----AEEQKR----- 360  
Db Db VPDSGPKSPDNHSTLKTVSTPNSTABEADHDLTEHNSPPLKAPLSTNPLHSDS 604  
QY QY -----GAPACAGSGTGTGTGA-----RSABEAPLYSKVTPR-----AQR 397  
Db Db DSDGSSDGAVERNTSISTASATVSPASSAESACTRAVLPMSIARQEVAGTPHSGAEK 664  
QY QY GAHARDARGTLPGV----- 413  
Db Db ADVSESPPLPERTFESFVLADMPVRPEWHLPNQWSEORSEGLTSGNEKHDAGGI 724  
QY QY -----ADQSPAGSGAYEDVA--GGAOTGGLGNLRIGRPGKPPDPAEWT 456  
Db Db HTASADSPAPFSDKDKQITKSPAETVDIGFNGRCGKPGPREPSEWT 773

RESULT 14  
US-10-366-547-77  
; Sequence 77, Application US/10366547  
; Publication No. US20030215899A1  
; GENERAL INFORMATION:  
; APPLICANT: Meng, Tzu-Ching  
; APPLICANT: Tonks, Nicholas K.  
; APPLICANT: Cool, Deborah E.  
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASES  
; FILE REFERENCE: 200125.439  
; CURRENT APPLICATION NUMBER: US/10/366,547  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 77  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-366-547-77

Query Match 29.1%; Score 705.5; DB 14; Length 382;  
Best Local Similarity 45.1%; Pred. No. 5.1e-49;  
Matches 133; Conservative 59; Mismatches 94; Indels 9; Gaps 4;  
QY 9 RSFLERLEA-----RGRGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYK 63  
Db 8 RRFIORVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGSKENVKKNRYK 65  
QY 64 DVLDPDQTRVILSLQEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLWFEFG 123  
Db 66 DILFPDHSRVKLTLPQSDSDYINANFIKGVYGPAYVATQGPLANTVIDFWRMIWEYN 125

DB Db ESRLYQHYVWPDHDPVSSFDSDILDMISLMRYQEHEDVPICHCSAGCGRTGACAI 244  
QY QY DYVROLLTQMIIPDPDFSLFVVKMKRQBPAAVOTESQYRFLYHTVQMF----- 292  
Db Db DYTWNLLKAGKIPBEFNVFNLIQEMRTORHSAVQTKQYELVHRAIAQLFKQQLQYVEIH 304  
QY QY -----C-----STLQNASPH----- 302  
Db Db GAKTIADGNEITGTMWSSIDSEKQDPPKPPRTRSCLVGEGDAKEEILQPEHPVPP 364  
QY QY -----Y 303  
Db Db LTPSPPSAFTVTVMQDSDRYHPKPVLMHDEQHPADLNRSYDKSADPMGKSEAIHID 424  
QY QY QNIKENCA-----PL-----YDALLFL-----RT--PQALLA----- 328  
Db Db KKLERNLSFEIKVPLQBGPKSFDGNTLLNKGHAIKKSSASSVVDRSKPQELSAGALK 484  
QY QY -----TPRP-----PGVLRSI-----S 341  
Db Db VDDVQNSCADCSAAHSHRAAESSEOSNSHTPPRDCPLDKKKGHVTVSLHGFENATP 544  
QY QY VPGSPGHAMADTY-----AEEQKR----- 360  
Db Db VPDSGPKSPDNHSTLKTVSTPNSTABEADHDLTEHNSPPLKAPLSTNPLHSDS 604  
QY QY -----GAPACAGSGTGTGTGA-----RSABEAPLYSKVTPR-----AQR 397  
Db Db DSDGSSDGAVERNTSISTASATVSPASSAESACTRAVLPMSIARQEVAGTPHSGAEK 664  
QY QY GAHARDARGTLPGV----- 413  
Db Db ADVSESPPLPERTFESFVLADMPVRPEWHLPNQWSEORSEGLTSGNEKHDAGGI 724  
QY QY -----ADQSPAGSGAYEDVA--GGAOTGGLGNLRIGRPGKPPDPAEWT 456  
Db Db HTASADSPAPFSDKDKQITKSPAETVDIGFNGRCGKPGPREPSEWT 773

RESULT 13  
US-10-322-281-845  
; Sequence 845, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 845  
; LENGTH: 773  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-322-281-845

Query Match 29.1%; Score 706; DB 16; Length 773;  
Best Local Similarity 25.5%; Pred. No. 1.2e-48;  
Matches 196; Conservative 86; Mismatches 163; Indels 324; Gaps 20;  
QY 9 RSFLERLEA-----RGRGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYK 63  
Db 8 RRFIORVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGSKENVKKNRYK 65  
QY 64 DVLDPDQTRVILSLQEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLWFEFG 123  
Db 66 DILFPDHSRVKLTLPQSDSDYINANFIKGVYGPAYVATQGPLANTVIDFWRMIWEYN 125  
QY 124 VKVILMACREIENGKRCERYH-AQEQLPQTGLFCITLIEKWLNEIDIMLRLTKVTFQX 182  
Db 126 VVIIWACREIFEMGRKKRCERYHPLYGDFITFAPFKISCENEQ-ARTDYFIRTLLEFQX 184  
QY 183 EBSRVYQLYQWSPDRGVPSPDHMLAMVVEARLQSGSPFLCVHCSAGCGRTGLCTV 242

QY 124 VKVILMACREIENGKRCERYW-AQOEPLQTGLFCITILIKEKWLNEIDIMLRLTKVTFQK 182  
Db 126 VVIIVMACREFENGKRCERYWPLYGEDPITAPFKISCENEQ-ARTDYFIRTLLEFQ 184  
QY 183 EGRSVYQLOVMGWPDRGVSSPDHMLAMVEEARLQSGSPPELVCVHCSAGCGRTGVLCTV 242  
Db 185 ESRRLYQPHYVNVWPDHDPSSFDSDILDMISLARKYQEHEDVPICHCSAGCGRTGAICAI 244  
QY 243 DYVRQLLLTQMPPDPFSLFDVVLKMKRQPPAAVQTEEQYRFLYHTVAQMFSTLQ 297  
Db 245 DYTWNLLKAGKIPPEEFNVNLIQEMKRTQHSVQTEQYELVHRAIAQLFEKQLQ 299

## RESULT 15

US-10-366-547-75  
; Sequence 75, Application US/10366547  
; Publication No. US20030215899A1  
; GENERAL INFORMATION:  
; APPLICANT: Meng, Tzu-Ching  
; APPLICANT: Tonks, Nicholas K.  
; APPLICANT: Cool, Deborah E.  
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASES  
; FILE REFERENCE: 200125.439  
; CURRENT APPLICATION NUMBER: US/10/366,547  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 75  
; LENGTH: 775  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-366-547-75

Query Match 29.0%; Score 703; DB 14; Length 775;  
Best Local Similarity 25.0%; Pred. No. 2.1e-48;  
Matches 194; Conservative 84; Mismatches 162; Indels 336; Gaps 17;

QY 9 RGFLELEA-----RGREGAVLAGEFSDIQACSAWKADGVCSTVAGSRPENVRKNRYK 63  
Db 8 RRFQIRVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKKNRYK 65  
QY 64 DVLPYDQTRVILSLLOEGHSDYINGNFIRGVDGSLAYIATOGPLPHTLDDFWRLVWEFG 123  
Db 66 DILFPDHSRVKLTLPSPQSDSYINANFIKGYGKAVYATQGPFRNIVDFWRMIWEYN 125  
QY 124 VKVILMACREIENGKRCERYW-AQOEPLQTGLFCITILIKEKWLNEIDIMLRLTKVTFQK 182  
Db 126 VVIIVMACREFENGKRCERYWPLYGEDPITAPFKISCENEQ-ARTDYFIRTLLEFQ 184  
QY 183 EGRSVYQLOVMGWPDRGVSSPDHMLAMVEEARLQSGSPPELVCVHCSAGCGRTGVLCTV 242  
Db 185 ESRRLYQPHYVNVWPDHDPSSFDSDILDMISLARKYQEHEDVPICHCSAGCGRTGAICAI 244  
QY 243 DYVRQLLLTQMPPDPFSLFDVVLKMKRQPPAAVQTEEQYRFLYHTVAQMFSTLQ----- 297  
Db 245 DYTWNLLKAGKIPPEEFNVNLIQEMKRTQHSVQTEQYELVHRAIAQLFEKQLQLEYIH 304  
QY 298 ----- 297  
Db 305 GAQKIRGNEITGTWVSSIDSEKQSDPPKPPRTRSCVLGEADAKEEILQPPEHPVPPI 364  
QY 298 -----NASP----- 301  
Db 365 LTPSPSPAPTPTVTWQDSRYHPKPVLMHNSPEQHPADLNRSYDKSADQWCKSESATIEH 424  
QY 302 -----HYQNIKENCAPLYDDALFLRT--EQA 325  
Db 425 IDKKLERNLSFEIKKVPQLQEGPKSPDGNLTLLNRGHAIKIKSASSSWD-----RTSKPQE 479  
QY 326 LLA-----IRP-----PGGVIRSI- 340  
Db 480 LSAGALKVDVDSQNSCADCSAAHSHRAESSEESQSNSTHTPPRDCPLDLKKGHVTVSLH 539

QY 341 -----SVPGSPGHAMADTY-----AEQKQK----- 360  
Db 540 GPNATPVDPSPDGKSPDNHRSQTLKTVSSTPNSTAEBAHDLTEHNSFLLKAPLSFTN 599  
QY 361 -----GAPAGAGSGTGTGTGA-----RSAEAPLYSKVTPR----- 393  
Db 600 PLHSDDDWHSDGSSDGAVTNRKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTP 659  
QY 394 ---AQRPGAHAEADARGTLPGRVP----- 413  
Db 660 HSGAEXDADVSESPPLPERTPESEFVLADMPVRPEWHLPNOEWSEQSEGLTTSGNE 719  
QY 414 -----ADQSPAGSGAYEDVA-GGAOTGGIGLGNLRIGRPGKPRDPPAEWT 456  
Db 720 KHDAGGIHTEASADSPAPSDKDKQITKSPAETVDIGFGNRCGKPKGPREPPEWT 775

Search completed: December 7, 2004, 09:55:32  
Job time : 63 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:13 ; Search time 40 Seconds  
(without alignments)  
1101.682 Million cell updates/sec

Title: US-10-087-993A-36  
Perfect score: 2424  
Sequence: 1 MRSLSARSFLERLEARG.....NLRIKPKPRPPPAETRW 458

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755.5	31.2	802	1 B44390	protein-tyrosine-p
2	710	29.3	773	1 JH0609	protein-tyrosine-p
3	709	29.2	780	1 JG1368	protein-tyrosine-p
4	705.5	29.1	382	1 S48748	protein-tyrosine-p
5	705	29.1	775	2 S55345	protein-tyrosine-p
6	491.5	20.3	1118	1 A49724	protein-tyrosine-p
7	475.5	19.6	595	1 A44390	protein-tyrosine-p
8	474	19.6	1711	1 A55148	protein-tyrosine-p
9	463	19.1	595	1 S20825	protein-tyrosine-p
10	462	19.1	926	1 A41105	protein-tyrosine-p
11	453	18.7	593	1 JN0805	protein-tyrosine-p
12	453	18.7	593	2 JG5167	protein-tyrosine-p
13	451	18.6	585	2 A46209	protein-tyrosine-p
14	449	18.5	597	1 A53593	protein-tyrosine-p
15	448	18.5	521	1 A44267	protein-tyrosine-p
16	448	18.5	913	1 A41109	protein-tyrosine-p
17	444	18.3	595	1 A56551	protein-tyrosine-p
18	442	18.2	694	2 A33978	protein-tyrosine-p
19	441	18.2	597	2 B33978	protein-tyrosine-p
20	435	17.9	1337	1 I38670	protein-tyrosine-p
21	431	17.8	398	2 T08716	protein-tyrosine-p
22	430.5	17.8	435	1 TPUH01	protein-tyrosine-p
23	430.5	17.8	832	2 JG8051	protein-tyrosine-p
24	430	17.7	593	1 A42690	protein-tyrosine-p
25	429.5	17.7	583	2 S17671	protein-tyrosine-p
26	428	17.7	624	2 T19630	hypothetical prote
27	428	17.7	1026	2 T19631	protein-tyrosine-p
28	426.5	17.6	802	1 A36065	protein-tyrosine-p
29	424.5	17.5	1437	2 T31093	probable protein-t

30 424.5 17.5 2490 1 A54971 protein-tyrosine-p  
31 424 17.5 1301 1 A41622 protein-tyrosine-p  
32 423.5 17.5 829 1 A47373 protein-tyrosine-p  
33 423 17.5 360 2 JH0692 protein-tyrosine-p  
34 421.5 17.4 1238 2 S68700 HFTP beta-like tyr  
35 421.5 17.4 2294 2 I67630 protein-tyrosine-p  
36 421.5 17.4 2466 2 I67629 probable protein-t  
37 421 17.4 1200 2 T43148 leukocyte antigen-  
38 420 17.3 1898 2 S46216 receptor tyrosine  
39 420 17.3 2051 2 T30938 protein-tyrosine-p  
40 419.5 17.3 1188 1 A57064 protein-tyrosine-p  
41 419.5 17.3 1216 2 S60613 protein-tyrosine-p  
42 419.5 17.3 1997 1 S12050 protein-tyrosine-p  
43 419 17.3 1442 1 B48148 protein-tyrosine-p  
44 419 17.3 1445 1 A48148 protein-tyrosine-p  
45 418.5 17.3 405 2 I49372 protein-tyrosine-p

ALIGNMENTS

RESULT 1

B44390 protein-tyrosine-phosphatase (EC 3.1.3.48) PEP, nonreceptor type 8 - mouse  
N:Alternate names: protein-tyrosine-phosphatase PEP  
C:Species: Mus musculus (house mouse)  
C:Date: 03-May-1994 #sequence revision 26-May-1994 #text\_change 09-Jul-2004  
C:Accession: B44390; S71952; S27876  
R:Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.  
Mol. Cell. Biol. 12, 2396-2405, 1992  
A:Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: c  
, and threonine-rich sequences.  
A:Reference number: A44390; MUID:92236615; PMID:1373816  
A:Accession: B44390  
A:Molecule type: mRNA  
A:Residues: 1-802 <MAT>  
A:Cross-references: UNIPROT:P29352; GB:M90388; NID:g200522; PIDN:AAA39994.1; PID:g200523  
R:Cloutier, J.F.; Veillette, A.  
EMBO J. 15, 4909-4918, 1996  
A:Title: Association of inhibitory tyrosine protein kinase p50(ck) with protein tyrosine  
A:Reference number: S71952; MUID:97045099; PMID:8890164  
A:Accession: S71952  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 495-789 <CLO>  
C:Comment: This protein is found primarily in hematopoietic tissues.  
C:Genetics:  
A:Gene: 70zpep  
C:Complex: physically associates with inhibitory tyrosine protein kinase Csk; interaction  
C:Function:  
A:Description: probably an effector and/or regulator of tyrosine protein kinase csk in T-  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphatase  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:54-278/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:497-802/Region: glutamic acid/proline/serine/threonine-rich  
F:613-621/Region: proline-rich  
F:688-695/Region: proline-rich  
F:227/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 31.2%; Score 755.5; DB 1; Length 802;  
Best Local Similarity 44.0%; Pred. No. 2.9e-47;  
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 ABEPSDIQCSAAWKGVCSTVAGSRPENKRYKQVLPYDQTRVILSLQEEGHSY 86  
Db 25 ASEFLKFKQSTKYKADKIPTTVAQRPKNIKNRYKDLIPYDHSILVELSLTSDSSY 84  
QY 87 INGNFIRGVDGSLAVIATQGPLPHTLLDFWRLWFEFGVKVILMACREINGRKRERYWA 146  
Db 85 INASFIKGYGPKAYIATQGPLSTLLDFWRLWFEYRILVIVMACNEFMGKKKERYWA 144  
QY 147 QEQE-PLQTGLFCITLLEKWLINELMTLKVTFQKESRSYVQLQYMWSPDRGVSSPD 205

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Db 145 EGETOLQGPSPISCEAEK-KKSDYKIKTLAKFNNETRIIYQHYKNWPDHDPSSID 203
Qy 206 HMLAMVEEARLQGSPEPLCHVCSAGCGRTGVLCTVDYVROLTLTQIMPDPFSLFVVL 265
Db 204 PILQLIWMRCYQEDDCVFCICHSAGCGRTGVCADVYTWMLLKDGIIKPNFSVENLIQ 263
Qy 266 KNRKQBPAAVCTEEOYRFLYHYVQMFCSCTLQASPHYQNIKENCAPLYDALLFRTPOA 325
Db 264 EMRTQPSLVQTEQYELYSVAVLELF-----KRHMDVSDNHLG-----REIQA 308
Qy 326 LLAIPRPPGGLVRSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTGTG 377
Db 309 QCSIFE-----QSLTVEADSCPLDLPKNAMEDVKTTHOHSKQGAESTGGSSIGLRTS 362
Qy 378 ARSAEE 383
Db 363 TMAEE 368

RESULT 2
JH0609
protein-tyrosine-phosphatase (EC 3.1.3.48) P19 - mouse
N;Alternate names: protein-tyrosine-phosphatase PTPY43
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: JH0609; PS0365; PS0369; PS0366; G61180
R;Den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A;Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
A;Reference number: JH0609; MUID:92272714; PMID:1590786
A;Accession: JH0609
A;Molecule type: mRNA
A;Residues: 1-773 <DEN>
A;Cross-references: GB:X63440; GB:S36169; NID:G416181; PIDN:CAA45037.1; PID:G416182
A;Experimental source: embryonic carcinoma cell, P19 cell
A;Accession: PS0365
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 88-91,'G','93-110,'G','112-118','S','120','T','122 <DE2>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone PTP33
A;Accession: PS0369
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 88-91,'G','93-109,'LG','112-120','T','122 <DE3>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone PTP59
A;Accession: PS0366
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 88-91,'KY','94-109,'LA','112-118','S','120-122 <DE4>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone PTP42
R;Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A;Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A;Reference number: A61180, MUID:92032882; PMID:1932742
A;Accession: G61180
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 124-127,'I','129-229 <YIA>
C;Comment: This protein is located in the cytoplasm.
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosphatase
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;55-229/Domain: phosphatase catalytic domain #status predicted <PCD>
F;58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
F;231/Active site: Cys (phosphotyrosine intermediate) #status predicted
F;237/Binding site: substrate phosphate (Arg) #status predicted

Query Match 29.3%; Score 710; DB 1; Length 773;
Best Local Similarity 25.4%; Pred. No. 5,8e-44;
Matches 195; Conservative 88; Mismatches 162; Indels 324; Gaps 20;
Qy 9 RSFLERLEA-----RGGREGAVLAGEFSDIQCSAAWKADGVCSTVAGSRPENVKRYK 63

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```

Db 8 RRIQVRQAMKSPDHNGEDN--PARDFMRLRLSTKYRTEKIYPTATGKEKEENVKKNRYK 65
Qy 64 DVLPTOTRVLSSLQEGHSDYINFGVVDGSLAYIATQGPLPHTLLDQWRLWBERG 123
Db 66 DILFDHRSRYKLTGKTPSDSDYINANFATKGVYKAYVATQPPFTVIDFWRMIWEYN 125
Qy 124 VKVILMACRIENGRKRCERYW-AQOEPLQTLGFCITLIKELWLNEDIMLRTLKVTFOK 182
Db 126 VMIWACREFFENGRKRCERYWPLYGEDFITAPFKISCENEQ-ARTDYFITLLLEFQN 184
Qy 183 ERSRVQLQVMSWPDGRGVSPDHMLAMVEEARLQGSPEPLCHVCSAGCGRTGVLCTV 242
Db 185 ESRLYQHYVNVWPDHDFSSFDISILDMISLRKYOEHEDEVPTICHCSAGCGRTGAICAI 244
Qy 243 DYVRQLLTQMIIPDFSLFDVVLKMKRKORPAAVQTEEOYRFLYHYTVQOMF----- 292
Db 245 DYTWNLLKAGKIPPEFNVFNLIQEMRTQHSVAOTKEQYELVHRAITAQLFENSYNCKEM 304
Qy 293 ----- 292
Db 305 EHRRSVVMWMLPLELWSVPLIARRDLAKAAADSKLPCRRGQGRNTTATRTSPGATHPD 364
Qy 293 -----CSTLQNAS-----PHYQN----- 305
Db 365 AITFSLPNVTVTCRTVGTGTSQCCCTWPHQSNQPTSTTEAMINORTNGAKSASEIHID 424
Qy 306 --IKENCA-----PI-----YDDALFL-----RT--PQALLA----- 328
Db 425 KKLERNLSPEIKKVPLOEGPKSFDGNTLLNRGHAIKIKSASSVVDRTSKPQELSAGALK 484
Qy 329 -----IPRP-----PGVLRSI-----S 341
Db 485 VDDVQNSCADCSAAHSHRAAESSESQSNSTPPRPDCLPLDKKHVTWLSLHGPENATP 544
Qy 342 VPGSPGHAMADTV-----AEEOKR----- 360
Db 545 VPDSPGKSPDNHSQTLKTVSTPSTAEAEADLTHEHNSPFLKAPLSFTNPLHSDDM 604
Qy 361 ---GAPAGAGSGTGTGTGA-----RSAEAPLYSKVTPR-----AQP 397
Db 605 HSDGSGSDGAVTRNKTSISTASATVSPASSASSACHRRVLPMSIARQAEVAGTPHSGAERD 664
Qy 398 GAHAEDARCTLPGRVP----- 413
Db 665 ADVSESPPLPERTPEPSFVLADMPVPRPWHELHPQEWSEQRESEGLTTSNGEKHDAGGI 724
Qy 414 ----ADQSPAGSGAYEDVA-GGAQTGGLGFLNLRIGRPKGRDPPAEWT 456
Db 725 HTEASADSPAFSDKKDQITKSPAETVDIGFNGRCGKPKGPREPSEWT 773

RESULT 3
JCI368
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN12, nonreceptor type 12 [validated] - human
N;Alternate names: PTP-PEST; PTPG1
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
A;Accession: JCI368; A47506; A45496; S41746
R;Takekawa, M.; Itoh, F.; Hinoda, Y.; Arimura, Y.; Toyota, M.; Sekiya, M.; Adachi, M.; In
Biochem. Biophys. Res. Commun. 189, 1223-1230, 1992
A;Title: Cloning and characterization of a human cDNA encoding a novel putative cytoplasm
A;Reference number: JCI368; MUID:93112015; PMID:1472029
A;Accession: JCI368
A;Molecule type: mRNA
A;Residues: 1-780 <TAK>
A;Cross-references: UNIPROT:Q05209; DBJ:DJ13380; NID:G220033; PIDN:BAA02648.1; PID:G22003
A;Note: the authors translated the codon AGT for residue 636 as Ala
R;Yang, Q.; Co, D.; Sommercorn, J.; Tonks, N.K.
J. Biol. Chem. 268, 17650, 1993
A;Reference number: A47506; MUID:93352561; PMID:8349645
A;Contents: erratum
A;Accession: A47506
A;Molecule type: mRNA

```



```

QY 124 VKVLMACREIENGKRCRYW-AQOEPLQTLGTCITLIKWKLNEDIMLTKVTKQ 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 VLIIVACREFEGRKRCRYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLEFQN 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 ERSVYQLOVMSPDRGVSSPDHMLAMVEARRLQSGPEPLVCHVCSAGCGRTGVLT 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 ESRLLQFHYVWPDHDVSSFDSDILDMISLKRKQEHEDVPICHSAGCGRTGAI 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 DYVRQLLLQMLPPDFSLFDVLMKRCORPAAVQTEQYRFLYHTVAQMFSTLQ- 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 DYTWNLLKAGKIPENFVNLQEMRQHSVQTKQYELVHRAIAQLFEKQLQLYBIH 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 ----- 297
Db 305 GAKIADGNEITGTWVSSIDSEKQDPPPKPPRTSRCLVGEADAKEILQPEHPVPI 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 ----- 301
Db 365 LTPSPSAPPTVTWQSDRYHPEKPVLVHVASPEQHPADLNRSYDKSADQMGKSESAIEH 424
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 ----- 325
Db 425 IDKKLERNLSPIKKVPLQEGPKSFDGNLTLLNRGHAIKIKSASSVWD-----RTSKPQE 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 326 LLA-----IPRP-----PGGLRSI- 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 LSGALKYDDVQNSCADSCAAHSHRAESSQSNSTHTPRPDCLPLDKKHVTWLSH 539
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 -----SVPGSPGHAMADTY-----AEEQKR----- 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 540 GPNATFVDPSPGKSPDNHQSOTLKTVSTPNTAEAAHDLTEHNSPLKAPLSFTN 599
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 -----GAPAGAGSGTGTGTGA-----RSABEAPLYSKVTR----- 393
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 600 PLHSDWHSDGSSDGAVTNRKNTSISTASATVSPASSAESCHRRVLPMSARQVAGTP 659
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 394 ---AQRFGAHEADARTGLGRVP----- 413
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 660 HSGAEXDADVSESPPLPERTPESPFLVADMPVRPEWHLPNQEWSEGESEGLTSGNE 719
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 414 -----ADQSPAGSAYEDVA-CGAQTGLGLNLRIGRKGRDRDPAEWT 456
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 720 KHDAGIHTASADSPFASDKXQITKSPAEVTDIGFNGRCGPKGPREPSEWT 775
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

## RESULT 6

```

A49724
N;Alternate names: protein-tyrosine-phosphatase, receptor type H precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: A49724
R;Matuzaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.
J. Biol. Chem. 269, 2075-2081, 1994
A;Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase an
A;Reference number: A49724; MUID:94124561; PMID:8294459
A;Accession: A49724
A;Molecule type: mRNA
A;Residues: 1-1118 <MAYO>
A;Cross-references: UNIPROT:Q15426; GB:D15049; NID:9475003; PIDN:BA003645.1; PID:g475004
C;Genetics:
A;Gene: GDB:PTPRH; SAP-1
A;Cross-references: GDB:305504
A;Map position: 19q13.4-19q13.4
A;Note: Highly expressed in colon and pancreatic cancer cells but not in the normal cell
C;Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repea
C;Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric monoox
F;1-27/Domain: signal sequence #status predicted <SIG>
F;27-110/Domain: fibronectin type III repeat homology <3FNB>
F;28-118/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <MAYO>
F;28-761/Domain: extracellular #status predicted <EXT>
F;116-199/Domain: fibronectin type III repeat homology <3FNB>

```

```

F;205-289/Domain: fibronectin type III repeat homology <3FNC>
F;296-379/Domain: fibronectin type III repeat homology <3FND>
F;385-468/Domain: fibronectin type III repeat homology <3FNE>
F;474-558/Domain: fibronectin type III repeat homology <3FNF>
F;564-658/Domain: fibronectin type III repeat homology <3FNG>
F;667-737/Domain: fibronectin type III repeat homology <3FNH>
F;762-778/Domain: transmembrane #status predicted <TMN>
F;779-1118/Domain: intracellular #status predicted <INT>
F;846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;35,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558,57
F;1022/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.3%; Score 491.5; DB 1; Length 1118;
Best Local Similarity 43.3%; Pred. No. 8.4e-28;
Matches 116; Conservative 36; Mismatches 91; Indels 25; Gaps 9;

QY 47 STVAGSRPENVRKRYKVDLPYDQTRVLSLQEEGSHSYINGNFRIGVDGSLAYIATQG 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 SQMVASASENNAKRYNVLPYDWSRVPLKPIHEEPGSDYINASFMPGLWSPQEFIAQ 896
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 PLDHTLLDFWLVWFGVKVILMACREIENGKRCRYWQAQOEPLQTLGTCITL- 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 897 PLPTQVGFVRLVWEOQSHTLVMLTNCMEAGRVKCHYWPDSQPCTHGLHRLVTLG 956
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 KERWLNEDIMLRLTKVTFQKESVYQLQYMSWPDGVSPDHMLAMVEARR-----L 217
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 957 MENWTVRELLL--LQVEEQK-TLSVRQFYQAWPDHGVSPSPDTLLAFWMLRQLWLD 1013
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 218 QSGSPPLVCHSAGCGRTGVLTVD-YVRQLLLQMIIPDPSLFDVLMKRCORPAAVQ 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1014 EGPPP---IVHCSAGVGRGTGLIALDVLLRQLQSEGLLGP---FSFVRMRRESR 1066
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 277 TEEQYRFLYHTVAQMFCSITLQNASPHYQ 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1067 TEAQYVFLH---QCICGS-SNSQPRPQ 1089
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
A44390
N;Alternate names: hematoopoietic cell phosphatase (HCP); protein-tyrosine-phosphatase 1C
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 19-May-1994 #text_change 11-Jun-1999
C;Accession: A44390; A42031; F61180; I65741; I52816; I65740; A45143; B45143
R;Matthews, R.J.; Bowne, D.B.; Fiores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A;Title: Characterization of hematoopoietic intracellular protein tyrosine phosphatases: c
   and threonine-rich sequences.
A;Reference number: A44390; MUID:92236615; PMID:1373816
A;Accession: A44390
A;Molecule type: mRNA
A;Residues: 1-595 <MAT>
A;Cross-references: GB:M90389; NID:9200550; PIDN:AAA40007.1; PID:g200551
R;Yi, T.L.; Cleveland, J.L.; Ihle, J.N.
Mol. Cell. Biol. 12, 836-846, 1992
A;Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferen
A;Reference number: A42031; MUID:92123209; PMID:1732748
A;Accession: A42031
A;Molecule type: mRNA
A;Residues: 1-595 <YIL>
A;Cross-references: GB:M68902; NID:g193807
A;Note: sequence extracted from NCBI backbone (NCBIN:76845, NCBI:76846)
R;Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A;Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A;Reference number: A61180; MUID:92032882; PMID:1932742
A;Accession: F61180
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 332-451 <YTA>
R;Snitza, L.D.; Schweitzer, P.A.; Rajan, T.V.; Yi, T.; Ihle, J.N.; Matthews, R.J.; Thomas
Cell 73, 1445-1454, 1993

```



A;Title: Mutations at the murine motheaten locus are within the hematopoietic cell prote  
A;Reference number: I52816; MUID:93313972; PMID:8324828  
A;Accession: I65741  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 334-353 359-382 <SHU1>  
A;Cross-references: GB:863803; NID:g388449  
A;Note: deletion mutation  
A;Accession: I52816  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 350-358 'EGSPNFLTPTFSSLVVQVHTQ' 359-366 <SHU2>  
A;Cross-references: GB:863763; NID:g388447  
A;Note: insertion mutation  
A;Accession: I65740  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 34-76 'VPRPIWRAGVTAAAGQGRALD' <SHU3>  
A;Cross-references: GB:863764; NID:g388450  
A;Note: frameshift mutation  
A;Yeung, Y.G.; Berg, K.L.; Pixley, F.J.; Angeletti, R.H.; Stanley, E.R.  
J. Biol. Chem. 267, 23447-23450, 1992  
A;Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in macroph  
A;Reference number: A45143; MUID:93054686; PMID:1385421  
A;Accession: A45143  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 137-139, 'X' 141-143, 'X' 145-151 <YE1>  
A;Experimental source: BAC1.2F5 macrophage  
A;Note: sequence extracted from NCBI backbone (NCBIP:118519)  
A;Accession: B45143  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 54-56, 'X' 58, 'X' 60-61, 'X' 63-68 <YE2>  
A;Experimental source: BAC1.2F5 macrophage  
A;Note: sequence extracted from NCBI backbone (NCBIP:118518)  
A;Comment: This protein is found primarily in hematopoietic tissues.  
C;Genetics:  
A;Gene: me/HCPH; motheaten  
C;Function:  
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to release phosphate  
A;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph  
A;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:4-98/Domain: SH2 homology <SH2A>  
F:110-211/Domain: SH2 homology <SH2B>  
F:265-521/Domain: phosphatase catalytic domain #status predicted <PHP>  
F:270-504/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:453/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:453/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 475.5; DB 1; Length 595;

Best Local Similarity 36.2%; Pred. No. 5.6e-27;

Matches 106; Conservative 53; Mismatches 105; Indels 29; Gaps 8;

QY 22 ECAVLAG---PESDIQACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSL 78  
DB 237 EDTAKAGFWBESLQ-----KQEVNKLHQRLEGORPENKSNRYNKLIPFDHNSVIL--- 289  
QY 79 QBEHG-----SDYINGNFIQV-----DGLAVIATQGLPHTLLDFWRLVWFEFGVKVI 127  
DB 290 --QGRDSNIPGSDYINANYVKNQLGPDENSKTYIASQGLDATVNDPFWQMAWQENTRVI 347  
QY 128 IMACREIENGKRCERYVAQOEPLQGLFCITLIKRWLNEDIMRLTKVTPKES--- 184  
DB 348 VMTTREVKGKNCVPYFPEVGTQRYVGLYSVTNSREHDTAE-YKLRVLTQISPLDNGDLV 406  
QY 185 RSVYQLQYMSWPDGRGVPSSPDHMLAMVEARRLOQSGPE--PLCVHCSAGCGRTGVLCTV 242  
DB 407 REIMHYQLSWPDHGVPEPGVLSFLQINQORQESLPHAGPIIVHCSAG:GRGTIIVI 466  
QY 243 DYVRQLLTQMTIPPFSLFDVVLKMKRKORPAAVQTEBOYRFLYHTVAQMFST 295  
DB 467 DMLMESISTKGLDCDIDIOKTIQTMVRAQSGMVQTEAQYKFIYVAIAQFIET 519

# RESULT 8

A55148  
A;Title: Mutations at the murine motheaten locus are within the hematopoietic cell prote  
A;Reference number: I52816; MUID:93313972; PMID:8324828  
A;Accession: I65741  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 334-353 359-382 <SHU1>  
A;Cross-references: GB:863803; NID:g388449  
A;Note: deletion mutation  
A;Accession: I52816  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 350-358 'EGSPNFLTPTFSSLVVQVHTQ' 359-366 <SHU2>  
A;Cross-references: GB:863763; NID:g388447  
A;Note: insertion mutation  
A;Accession: I65740  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 34-76 'VPRPIWRAGVTAAAGQGRALD' <SHU3>  
A;Cross-references: GB:863764; NID:g388450  
A;Note: frameshift mutation  
A;Yeung, Y.G.; Berg, K.L.; Pixley, F.J.; Angeletti, R.H.; Stanley, E.R.  
J. Biol. Chem. 267, 23447-23450, 1992  
A;Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in macroph  
A;Reference number: A45143; MUID:93054686; PMID:1385421  
A;Accession: A45143  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 137-139, 'X' 141-143, 'X' 145-151 <YE1>  
A;Experimental source: BAC1.2F5 macrophage  
A;Note: sequence extracted from NCBI backbone (NCBIP:118519)  
A;Accession: B45143  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 54-56, 'X' 58, 'X' 60-61, 'X' 63-68 <YE2>  
A;Experimental source: BAC1.2F5 macrophage  
A;Note: sequence extracted from NCBI backbone (NCBIP:118518)  
A;Comment: This protein is found primarily in hematopoietic tissues.  
C;Genetics:  
A;Gene: me/HCPH; motheaten  
C;Function:  
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to release phosphate  
A;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph  
A;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:4-98/Domain: SH2 homology <SH2A>  
F:110-211/Domain: SH2 homology <SH2B>  
F:265-521/Domain: phosphatase catalytic domain #status predicted <PHP>  
F:270-504/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:453/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:453/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 474; DB 1; Length 1711;

Best Local Similarity 39.9%; Pred. No. 2.7e-26;

Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;

QY 10 SFLELEARGREGAVLAGESFDIOACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYD 69  
DB 1134 SPFQSYEAKSAHAHQTFQFEELKEVGKQ-----PRLAEHPDNIKORYPHVLVYD 1187  
QY 70 QTRVILSLLOEBGHSDYINGNFIQVGDGSLAYIATQGLPHTLLDFWRLVWFEFGVKVILM 129  
DB 1188 HSRVLTQLPGEPHSDYINANFIPGYSHTQETIATQGLPKKTLEDFWRLVWFEQVHVILM 1247  
QY 130 ACREIENGKRCERYVAQOEPLQGLFCITLIKE-----KWLNEIMRLTKLVTPKESR 185  
DB 1248 LTVGMENGRVLCHEHYWPANSTVTHGHITIHLLABEPEDEMTREFFLQ--HGTSQKQ-R 1304  
QY 186 SVYQLQYMSWPDGRGVPSSPDHMLAMV---BEARLOQSGPPLCVHCSAGCGRTGVLCT 241  
DB 1305 RVKQLQFTTWPDSHVSPEAPSSLLAFVELVQEQVQATQKG--PILVHCSAGVGRGT--- 1359  
QY 242 VDYVRQLLTQMTIPPD--FSLFDVVLKMKRKORPAAVQTEBOYRFLY 285  
DB 1360 --FVALLRLRLQLEBEKQADVNTVYILRLHPLMIQILSQYIFLH 1403

# RESULT 9

S20825

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN6, nonreceptor type 6 [validated] - human  
N;Alternate names: hematopoietic cell phosphatase HCP; protein-tyrosine-phosphatase 1C; i  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence revision 08-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: B42031; A38189; S20825; S17234; S20837  
R;Yi, T.L.; Cleveland, J.L.; Ihle, J.N.  
Mol. Cell. Biol. 12, 836-846, 1992  
A;Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferen  
A;Reference number: A42031; MUID:92123209; PMID:1732748  
A;Accession: B42031  
A;Molecule type: mRNA  
A;Residues: 1-595 <Y1>  
A;Cross-references: UNIPROT:P29350; GB:M74093  
A;Experimental source: T-lymphoid cell line  
A;Note: sequence extracted from GenBank  
R;Plutsky, J.; Neel, B.G.; Rosenberg, R.D.  
Proc. Natl. Acad. Sci. U.S.A. 89, 1123-1127, 1992  
A;Title: Isolation of a src homology 2-containing tyrosine phosphatase.  
A;Reference number: A38189; MUID:92141214; PMID:1736296

Query Match 19.6%; Score 475.5; DB 1; Length 595;

Best Local Similarity 36.2%; Pred. No. 5.6e-27;

Matches 106; Conservative 53; Mismatches 105; Indels 29; Gaps 8;

QY 22 ECAVLAG---PESDIQACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSL 78  
DB 237 EDTAKAGFWBESLQ-----KQEVNKLHQRLEGORPENKSNRYNKLIPFDHNSVIL--- 289  
QY 79 QBEHG-----SDYINGNFIQV-----DGLAVIATQGLPHTLLDFWRLVWFEFGVKVI 127  
DB 290 --QGRDSNIPGSDYINANYVKNQLGPDENSKTYIASQGLDATVNDPFWQMAWQENTRVI 347  
QY 128 IMACREIENGKRCERYVAQOEPLQGLFCITLIKRWLNEDIMRLTKVTPKES--- 184  
DB 348 VMTTREVKGKNCVPYFPEVGTQRYVGLYSVTNSREHDTAE-YKLRVLTQISPLDNGDLV 406  
QY 185 RSVYQLQYMSWPDGRGVPSSPDHMLAMVEARRLOQSGPE--PLCVHCSAGCGRTGVLCTV 242  
DB 407 REIMHYQLSWPDHGVPEPGVLSFLQINQORQESLPHAGPIIVHCSAG:GRGTIIVI 466  
QY 243 DYVRQLLTQMTIPPFSLFDVVLKMKRKORPAAVQTEBOYRFLYHTVAQMFST 295  
DB 467 DMLMESISTKGLDCDIDIOKTIQTMVRAQSGMVQTEAQYKFIYVAIAQFIET 519

A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-tyr  
 A:Reference number: A41105; MUID:91288564; PMID:1648233  
 A:Accession: A41105  
 A:Molecule type: mRNA  
 A:Residues: 1-85; V, 87-595 <PLU>  
 A:Cross-references: GB:M77273; PIDN:G338079; PIDN:AAA36610.1; PID:G338080  
 A:Note: sequence extracted from NCBI backbone (NCBIN:79619, NCBI:79620)  
 R:Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.  
 Nature 353, 868, 1991  
 A:Title: Corrigendum: A protein-tyrosine phosphatase with sequence similarity to the SH2  
 A:Reference number: S20825  
 A:Accession: S20825  
 A:Molecule type: mRNA  
 A:Residues: 1, 'LSRG', 4-595 <SHE>  
 A:Cross-references: EMBL:X62055; NID:G35781; PIDN:CAA43982.1; PID:G35782  
 R:Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.  
 Nature 352, 736-739, 1991  
 A:Title: A protein-tyrosine phosphatase with sequence similarity to the SH2 domain of th  
 A:Reference number: S17234; MUID:91343005; PMID:1652101  
 A:Accession: S17234  
 A:Molecule type: mRNA  
 A:Residues: 1, 'LSRG', 4-589, 'VPSRGSRCCPQVAMPQ' <SH2>  
 A:Experimental source: breast carcinoma cells  
 A:Note: sequence revised in reference S20805  
 C:Genetics:  
 A:Gene: GDB:PTPN4  
 A:Cross-references: GDB:131389; OMIM:176883  
 A:Map position: 12p13-12p13  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:4-98/Domain: SH2 homology <SH2>  
 F:110-211/Domain: SH2 homology <SH2B>  
 F:265-521/Domain: phosphatase catalytic domain #status predicted <PHP>  
 F:270-504/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:453/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:459/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.1%; Score 463; DB 1; Length 595;  
 Best Local Similarity 32.9%; Pred. No. 4.6e-26;  
 Matches 112; Conservative 56; Mismatches 110; Indels 62; Gaps 10;

Qy 22 EGAVLAG--EFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLSLL 78  
 Db 237 EDTAKAGWEEFESLQ----KQEVKULHQRLEQGRPENKGRKRYKNILPFDHRSVIL--- 289

Qy 79 QECH-----SDYINGNIRGV-----DGLAYATATGPLPHLLDFWRLWGEVVKVI 127  
 Db 290 --QGRDSNIPGSDYINANYKQLLGPDENAKTYIASQCLEATVNDPQWAWQNSRVI 347

Qy 128 LMACREIENGRKRCRYWAQOEPLQTGLFCITLKEKWLNEIDMLRLTKVTFQKES--- 184  
 Db 348 VMTREVEGRNKCVPYWEVGVQRAYGYSVTNCGEDHTE-YKLRITLQVSLDNGDLI 406

Qy 185 RSVYQLQYNSWPDGRGVPSSPDHMLAMVEARLQSGPB--PLCVHCSAGCGRTGVLCTV 242  
 Db 407 RETWHYQYLSWPDGHPSPGGVLSPLDQINQRESLPHAGPIIVHCSAG:GRGTITVI 466

Qy 243 DYVROLLLTQMIPDPSPDFVLLKMKRKQRPAAVQTEBOYRFLYHVAQMFCST----- 295  
 Db 467 DMLMENISTKGLDCDIDIOKTQWPAQSGMVGVEAQYKFIYVAIAQFIETTKKLEVL 526

Qy 296 -----LONA-----SPHYNIKEN 309  
 Db 527 QSQKGQSEYGNITYPPAMKNAHAKASRTSSKHEDVYEN 566

RESULT 10  
 A41105  
 N:protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human  
 N:Alternate names: PTPase MEG  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Mar-1992 #sequence\_revision 02-May-1994 #text\_change 09-Jul-2004  
 A:Accession: A41105  
 R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991

A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-tyr  
 A:Reference number: A41105; MUID:91288564; PMID:1648233  
 A:Accession: A41105  
 A:Molecule type: mRNA  
 A:Residues: 1-926 <GUA>  
 A:Cross-references: UNIPROT:P29074; GB:M68941; NID:G190747; PIDN:AAA36530.1; PID:G190748  
 A:Experimental source: megakaryocytes, cell line MEG-10  
 C:Genetics:  
 A:Gene: GDB:PTPN4  
 A:Cross-references: GDB:131387; OMIM:176878  
 A:Map position: 9q31-9q31  
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>  
 F:523-597/Domain: GLGF domain homology <GLG>  
 F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:852/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:858/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.1%; Score 462; DB 1; Length 926;  
 Best Local Similarity 37.6%; Pred. No. 9.4e-26;  
 Matches 106; Conservative 47; Mismatches 107; Indels 22; Gaps 9;

Qy 17 ARGREGAVLAGESFDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLS 76  
 Db 647 AEGLTGTGVLIT-QFDQYR-----KPGMTMCA-KLPQNIKNRYRDISPDATRVILL 698

Qy 77 LLOEGHSDYINGNIRGVDSGLA----YIATGPLPHLLDFWRLWGEVVKVILMACR 132  
 Db 699 ----KGNEDYINANYINMEIPSSIIINQYIACGPLPHCTDFWQMTWEGSSMVVMLTT 754

Qy 133 EIENGRKRCRYWAQOEPLQTGLFCITLKEKWLNEIDMLRLTKVTFQK--ESRSVYQL 190  
 Db 755 QVSRGRVKCHQYWPPTGSSSYCYQVTCHEEG-NTAYIFRQMTLFNQEKESRELTQI 813

Qy 191 QYNSWPDGRGVPSPDFHMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLCTVDYVRQLLL 250  
 Db 814 QYLAHPDHGVDDSSDFDFVCHVRNKRAGKEPVPVHCSAGIGRTGVLITME--TAMCL 871

Qy 251 TQMPDPDFSLFVLLKMKRKQRPAAVQTEBOYRFLYHVAQM 292  
 Db 872 IECNQVYPL-DIVRTWRDQRAMMIQTPSYRPFVCEAILKVY 912

RESULT 11  
 JN0805  
 N:protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN11, nonreceptor type 11 [validated] - huma  
 N:Alternate names: BPTP-3; protein-tyrosine-phosphatase SHP-2; PTP1D; PTP2C; SH-PTP2; SH-  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Mar-1994 #sequence\_revision 19-May-1994 #text\_change 09-Jul-2004  
 A:Accession: JN0805; A46210; A47386; A47244; S273398; C44329; S31767  
 R:Bastien, L.; Ramachandran, C.; Liu, S.; Adam, M.  
 Biochem. Biophys. Res. Commun. 196, 124-133, 1993  
 A:Title: Cloning, expression and mutational analysis of SH-PTP2, human protein-tyrosine I  
 A:Reference number: JN0805; MUID:94029983; PMID:8216283  
 A:Accession: JN0805  
 A:Molecule type: mRNA  
 A:Residues: 1-593 <BAS>  
 A:Cross-references: UNIPROT:Q06124; GB:I07527; NID:G292406; PIDN:AAA17022.1; PID:G292407  
 R:Vogel, W.; Lammers, R.; Huang, J.; Ullrich, A.  
 Science 259, 1611-1614, 1993  
 A:Title: Activation of a phosphotyrosine phosphatase by tyrosine phosphorylation.  
 A:Reference number: A46210; MUID:93206095; PMID:7681217  
 A:Accession: A46210  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-593 <VOG>  
 A:Cross-references: EMBL:X70766; NID:G35783; PIDN:CAA50045.1; PID:G35784  
 A:Experimental source: SK-BR-3 mammary carcinoma cells  
 A:Note: sequence extracted from NCBI backbone (NCBI:127775)  
 R:Almad, S.; Banville, D.; Zhao, Z.; Fischer, E.H.; Shen, S.H.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 2197-2201, 1993  
 A:Title: A widely expressed human protein-tyrosine phosphatase containing src homology 2

A;Reference number: A47386; MUID:93211929; PMID:7681589  
A;Accession: A47386  
A;Molecule type: mRNA  
A;Residues: 1-593 <AHM>  
A;Experimental source: umbilical cord  
A;Note: sequence extracted from NCBI backbone (NCBIN:128129, NCBIP:128131)  
R;Freeman Jr., R.M.; Plutsky, J.; Neal, B.G.  
Proc. Natl. Acad. Sci. U.S.A. 89, 11239-11243, 1992  
A;Title: Identification of a human src homology 2-containing protein-tyrosine-phosphatase  
A;Reference number: A47244; MUID:93087502; PMID:1280823  
A;Accession: A47244  
A;Molecule type: mRNA  
A;Residues: 1-593 <PRE>  
A;Cross-references: GB:L03535; NID:G338081; PIDN:AAA36611.1; PID:G338082  
A;Note: sequence extracted from NCBI backbone (NCBIN:119760, NCBIP:119761)  
R;Adachi, M.; Sekiya, M.; Miyachi, T.; Matsuno, K.; Hinoda, Y.; Imai, K.; Yachi, A.  
FEBS Lett. 314, 335-339, 1992  
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase SH-PTP3 with sequence  
A;Reference number: S27398; MUID:93106179; PMID:1281790  
A;Accession: S27398  
A;Molecule type: mRNA  
A;Residues: 1-534; R, 536-547, P, 549-593 <AD2>  
A;Cross-references: DDB:D13540; NID:G220071; PIDN:BAA02740.2; PID:G4519425  
R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yachi, A.  
Cancer Res. 52, 737-740, 1992  
A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.  
A;Reference number: A44329; MUID:92119637; PMID:1370651  
A;Accession: C44329  
A;Molecule type: mRNA  
A;Residues: 1-370-460 <ADA>  
A;Cross-references: GB:S78088; NID:G243547; PIDN:AAB21148.1; PID:G243548  
A;Experimental source: pre-B cell NALM-6  
A;Note: sequence extracted from NCBI backbone (NCBIN:78088, NCBIP:78089)  
A;Note: the authors did not report the entire codon for residue 92  
C;Comment: This ubiquitous enzyme plays a critical role in regulating physiological cell  
C;Genetics:  
A;Gene: GDB:PTFN11  
A;Cross-references: GDB:137093; OMIM:176876  
A;Map position: 12q24.1-12q24.1  
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase  
C;Keywords: phosphoprotein, phosphoric monoester hydrolase, tyrosine-specific phosphatase  
F;6-100/Domain: SH2 homology <SH2A>  
F;112-214/Domain: protein-tyrosine-phosphatase homology <PTP>  
F;273-510/Domain: protein-tyrosine-phosphatase homology <PTP>  
F;459/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;465/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.7%; Score 453; DB 1; Length 593;  
Best Local Similarity 33.8%; Pred. No. 2.4e-25;  
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;

QY 1 MSRLDSARGFLERLEARGREGAVLA-----GFSDI--QACSAANKADGVCS 47  
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQQECKLLY-----S 264

QY 48 TVAGSRPENVRNKRKYDQTRVILSLLOEGH-----SDYINGNFI-----RG 94  
DB 265 RKEGQRQENKNRKNILPFDHTRVVL-----HDGDPNEPVSVDYINANIIMPEFTKCNN 320

QY 95 VDGLAYIATOGPLPHTLLDPRVLWFGVKVILMACREIENGKRCERYWAOEQPLOT 154  
DB 321 SKPKKSYIATOGCLQNTVDFWRVFNQNSRVIVMTTKEVERGSKCKVYWPDEYALKEY 380

QY 155 GLFCITLKEKWLNEIMRLTKVTFQKE---SRSVYQLYMSWPDRCVPSSPDHMLAMV 211  
DB 381 GWMRVNPKES-AAHDYTLRELKLSKVQGGTERTVWQYHFTWPDHGVDPDGGVLDLFL 439

QY 212 BEARLQGS--GPPLCVHCSAGCGRTGLCTVDYVQRLLTQMIPPDFSLFDVLKMKR 269  
DB 440 EGVHKKQESIMDAGPVVHCSAGIGRTGTFIVIDILIDIREKGVDCDIDVPKTIQMVRS 499

Query Match 18.7%; Score 453; DB 1; Length 593;  
Best Local Similarity 33.8%; Pred. No. 2.4e-25;  
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;

QY 1 MSRLDSARGFLERLEARGREGAVLA-----GFSDI--QACSAANKADGVCS 47  
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQQECKLLY-----S 264

QY 48 TVAGSRPENVRNKRKYDQTRVILSLLOEGH-----SDYINGNFI-----RG 94  
DB 265 RKEGQRQENKNRKNILPFDHTRVVL-----HDGDPNEPVSVDYINANIIMPEFTKCNN 320

QY 95 VDGLAYIATOGPLPHTLLDPRVLWFGVKVILMACREIENGKRCERYWAOEQPLOT 154  
DB 321 SKPKKSYIATOGCLQNTVDFWRVFNQNSRVIVMTTKEVERGSKCKVYWPDEYALKEY 380

QY 155 GLFCITLKEKWLNEIMRLTKVTFQKE---SRSVYQLYMSWPDRCVPSSPDHMLAMV 211  
DB 381 GWMRVNPKES-AAHDYTLRELKLSKVQGGTERTVWQYHFTWPDHGVDPDGGVLDLFL 439

QY 212 BEARLQGS--GPPLCVHCSAGCGRTGLCTVDYVQRLLTQMIPPDFSLFDVLKMKR 269  
DB 440 EGVHKKQESIMDAGPVVHCSAGIGRTGTFIVIDILIDIREKGVDCDIDVPKTIQMVRS 499

QY 270 QRPAAVQTEQRYFLYHTVAGMFCSTLQ-----NASPHYQNIKENCA 311

DB 500 QRSQWQTEAQRYFIYMAV-QHYIETLQRRIEEBQSKRKGHEYNIKYSLA 550

RESULT 12

JC5167  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - chicken  
N;Alternate names: phosphotyrosine phosphatase; PTP1D; PTP2C; SH-PTP2; SyP  
C;Species: Gallus gallus (chicken)  
C;Date: 21-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: JC5167  
R;Park, C.Y.; LaMontagne, K.R.; Tonks, N.K.; Hayman, M.J.  
Gene 177, 93-97, 1996  
A;Title: Cloning and expression of the chicken protein tyrosine phosphatase SH-PTP2.  
A;Reference number: JC5167; MUID:97080506; PMID:8921851  
A;Contents: erythroblast  
A;Accession: JC5167  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-593 <PAR>  
A;Cross-references: UNIPROT:Q90687; GB:U38620; NID:G1054939; PIDN:AAC60049.1; PID:G105494;  
C;Comment: This enzyme plays positive roles in mitogenic signaling and early development.  
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase  
C;Keywords: phosphoprotein, phosphoric monoester hydrolase, tyrosine-specific phosphatase  
F;6-100/Domain: SH2 homology <SH2A>  
F;112-214/Domain: SH2 homology <SH2B>  
F;273-510/Domain: protein-tyrosine-phosphatase homology <PTP>  
F;559-570/Region: proline-rich  
F;459/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;465/Binding site: substrate phosphate (Arg) #status predicted  
F;542,547,580/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.7%; Score 453; DB 2; Length 593;  
Best Local Similarity 33.9%; Pred. No. 2.4e-25;  
Matches 118; Conservative 53; Mismatches 123; Indels 54; Gaps 12;

QY 1 MSRLDSARGFLERLEARGREGAVLA-----GFSDI--QACSAANKADGVCS 47  
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQQECKLLY-----S 264

QY 48 TVAGSRPENVRNKRKYDQTRVILSLLOEGH-----SDYINGNFI-----RG 94  
DB 265 RKEGQRQENKNRKNILPFDHTRVVL-----HDGDPNEPVSVDYINANIIMPEFTKCNN 320

QY 95 VDGLAYIATOGPLPHTLLDPRVLWFGVKVILMACREIENGKRCERYWAOEQPLOT 154  
DB 321 SKPKKSYIATOGCLQNTVDFWRVFNQNSRVIVMTTKEVERGSKCKVYWPDEYSLKEY 380

QY 155 GLFCITLKEKWLNEIMRLTKVTFQKE---SRSVYQLYMSWPDRCVPSSPDHMLAMV 211  
DB 381 GWMRVNPKES-AAHDYTLRELKLSKVQGGTERTVWQYHFTWPDHGVDPDGGVLDLFL 439

QY 212 BEARLQGS--GPPLCVHCSAGCGRTGLCTVDYVQRLLTQMIPPDFSLFDVLKMKR 269  
DB 440 EGVHKKQESIMDAGPVVHCSAGIGRTGTFIVIDILIDIREKGVDCDIDVPKTIQMVRS 499

QY 270 QRPAAVQTEQRYFLYHTVAGMFCSTLQ-----NASPHYQNIK 307  
DB 500 QRSQWQTEAQRYFIYMAV-QHYIETLQRRIEEBQSKRKGHEYNIK 546

RESULT 13

A46209  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - mouse  
N;Alternate names: SH-PTP; SH2-containing phosphotyrosine phosphatase SyP  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A46209  
R;Feng, G.S.; Hui, C.C.; Pawson, T.  
Science 259, 1607-1611, 1993  
A;Title: SH2-containing phosphotyrosine phosphatase as a target of protein-tyrosine kinase  
A;Reference number: A46209; MUID:93206094; PMID:8096088  
A;Accession: A46209

A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid

A:Residues: 1-585 <REN>

A:Cross-references: UNIPROT:P35235

A>Note: sequence extracted from NCBI backbone (NCBIP:127770)

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:6-100/Domain: SH2 homology <SH2A>

F:112-214/Domain: SH2 homology <SH2B>

F:273-514/Domain: protein-tyrosine-phosphatase homology <PTP>

F:463/Active site: Cys (phosphocysteine intermediate) #status predicted

F:469/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.6%; Score 451; DB 2; Length 585;  
Best Local Similarity 31.0%; Pred. No. 3.4e-25;  
Matches 128; Conservative 59; Mismatches 142; Indels 84; Gaps 15;

QY 1 MRSLSARSFLERLEARGREGAVLA-----GEFSDI--QACSAAWKADGVCS 47  
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDVKQGFWEFETLQQQCKLLY-----S 264

QY 48 TVAGSPENVRNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94  
DB 265 RREGQENKRNRYKNILPFDHTRVIL-----HDGDPNPSVDYINANIIMPEFETKCNN 320

QY 95 VDGSLAYIATQGLPHTLLDFWRLVWFGVKVILMACREINGRKRRCRYWAQOEPLQT 154  
DB 321 SKPKSYIATQGLQNTVDFWRFVQENSRVIVMTKEVERGSKCKVKYWPDEYALKEY 380

QY 155 GLFCITLKEKWLNEIMLRTLKVTFOKES-----RSVYQLYMSWPDGVSPSDHM 207  
DB 381 GVMRVNVRKES-AAHDYTLRELKLSKVGQALLQGNTERVTWQYHFTWPDHGVSPDGGV 439

QY 208 LAMVEEARLQGS--GPEPLCVHCSAGCGRTGLCTVDYVROLLTOMIPDFSLFDVYL 265  
DB 440 LDFLEEVHKKQESIVDAGPVVHCSAGIGRTGTFIVIDLIIREKGVDCIDVPTKI 499

QY 266 KMRKORPAAVQTEBQYRFLYHTVAQMFCSLTQ-----NASPHYONIKENCAPLYD 315  
DB 500 MVRSORSGMVQTEAQYRFYIMAV-QHYIETLQRREEQSKRKGHEYTNIK-----YS 552

QY 316 DALFLRTPQALLAI PRPPGVLRSIVPGSPGHAVADTVABEQKRGAPAGAGS 368  
DB 553 GELGYTETRV-----GCPGHSVSP--MDEVGQWVEGLGT 585

#### RESULT 14

A53593

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - rat

N:Alternate names: PTPase L1

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: A53593; S29281

R:Mei, L.; Doherty, C.A.; Huganir, R.L.

J. Biol. Chem. 269, 12254-12262, 1994

A>Title: RNA splicing regulates the activity of a SH2 domain-containing protein tyrosine

A:Reference number: A53593; MUID:94216346; PMID:7512964

A:Accession: A53593

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-597 <MEI>

A:Cross-references: UNIPROT:P41499; GB:U05963; NID:G458332; PIDN:AAAL19133.1; PID:G458333

R:Hiraga, A.; Munakata, H.; Hata, K.; Suzuki, Y.; Tsuki, S.

Eur. J. Biochem. 209, 195-206, 1992

A>Title: Purification and characterization of a rat liver protein-tyrosine phosphatase

A:Reference number: S29281; MUID:93011127; PMID:1382983

A:Accession: S29281

A:Molecule type: protein

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosine

F:6-100/Domain: SH2 homology <SH2A>

F:112-214/Domain: SH2 homology <SH2B>

F:273-514/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:463/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:469/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.5%; Score 449; DB 1; Length 597;  
Best Local Similarity 32.4%; Pred. No. 4.8e-25;  
Matches 125; Conservative 58; Mismatches 141; Indels 62; Gaps 14;

QY 1 MRSLSARSFLERLEARGREGAVLA-----GEFSDI--QACSAAWKADGVCS 47  
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDVKQGFWEFETLQQQCKLLY-----S 264

QY 48 TVAGSPENVRNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94  
DB 265 RREGQENKRNRYKNILPFDHTRVIL-----HDGDPNPSVDYINANIIMPEFETKCNN 320

QY 95 VDGSLAYIATQGLPHTLLDFWRLVWFGVKVILMACREINGRKRRCRYWAQOEPLQT 154  
DB 321 SKPKSYIATQGLQNTVDFWRFVQENSRVIVMTKEVERGSKCKVKYWPDEYALKEY 380

QY 155 GLFCITLKEKWLNEIMLRTLKVTFOKES-----RSVYQLYMSWPDGVSPSDHM 207  
DB 381 GVMRVNVRKES-AAHDYTLRELKLSKVGQALLQGNTERVTWQYHFTWPDHGVSPDGGV 439

QY 208 LAMVEEARLQGS--GPEPLCVHCSAGCGRTGLCTVDYVROLLTOMIPDFSLFDVYL 265  
DB 440 LDFLEEVHKKQESIVDAGPVVHCSAGIGRTGTFIVIDLIIREKGVDCIDVPTKI 499

QY 266 KMRKORPAAVQTEBQYRFLYHTVAQMFCSLTQ-----NASPHYONIKENCAPLYD 315  
DB 500 MVRSORSGMVQTEAQYRFYIMAV-QHYIETLQRREEQSKRKGHEYTNIK-----LVD 555

QY 316 DALFLRTPQALLAI PRPPGVLRSIS 341  
DB 556 QTSGDQSPILP-PCPTPPCAEMREDS 580

#### RESULT 15

A44267

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - slime mold (Dictyostelium)

C:Species: Dictyostelium discoideum

C>Date: 30-Apr-1993 #sequence\_revision 08-Mar-1996 #text\_change 24-Apr-1998

C:Accession: A44267

R:Howard, P.K.; Sefton, B.M.; Firtel, R.A.

Cell 71, 637-647, 1992

A>Title: Analysis of a spatially regulated phosphotyrosine phosphatase identifies tyrosine

A:Reference number: A44267; MUID:93046662; PMID:1423620

A:Accession: A44267

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA; DNA

A:Residues: 1-521 <HOW>

A>Note: sequence extracted from NCBI backbone (NCBIP:117713)

C:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:121-459/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>

F:310/Active site: Cys (phosphocysteine intermediate) #status predicted

F:316/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.5%; Score 448; DB 1; Length 521;  
Best Local Similarity 29.0%; Pred. No. 4.8e-25;  
Matches 113; Conservative 53; Mismatches 88; Indels 136; Gaps 13;

QY 44 GVCSTVAGSRPENVRNRYKDVLPYDQTRVILSLQEGHSDYINGNFRGVGSL--AY 101  
DB 109 GPSETSEGDKKHNTSKNRYTNILPVNHTVQLKIQDKGSDYINANYI---DGAVPKQF 165

QY 102 IATQGLPHTLLDFWRLVWFGVKVILMACREINGRKRRCRYWAQOEPLQTGF--- 157  
DB 166 ICTQGLPHTIADFWRNWENCRILVLMRSRNCRIKDXRWPEQTCGEFSGYNGN 225

QY 158 -----CITLIKELWLNEDIMLTKVTFQKESRYQLYMSWPDGVSPSDH-- 206  
DB 226 EVFGTYSVELVEIQDP--EREITITNRLTTEGETRDTIQYEGWPDHNI---PDHTQ 280

Qy	207	-----MLAMVEEARLQSGPE--PLCVHCSACGRTGVLCTV-----DYVRQLLT	251
Db	281	PFQLLHSITNRQNIIPSSDRNVPPIVHCSAGVGTGTCTAVIMMKLDHYFKOLDAT	340
Qy	252	---QMIPP-----	256
Db	341	PIDQVDPFTHLPI TEVQSDNLDKGLGYHFKSSIYNSNGINNNNNNNNNNNNNNNNN	400
Qy	257	-----DPSLPDVVLKVRKORPAAVQTEBOY	281
Db	401	GSNNTPQTEPNNEEDDDAAESTKYAIMDKYNSRIDFNLSIVLKLREQPGMWQOLEQY	460
Qy	282	RELYTV-AQMF---CSTLQNASPHYQNI	306
Db	461	LFCKYILAEIYHRLNCK-LGFSLPVNNI	489

Search completed: December 7, 2004, 09:50:20  
Job time : 43 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 7, 2004, 09:54:33 ; Search time 21 Seconds  
(without alignments)  
1446.364 Million cell updates/sec

Title: US-10-087-993A-36  
Perfect score: 458  
Sequence: 1 MSRLDSARSFLERLEARGG.....NLIRGPKGRDPDPAETWTRV 458

Scoring table: Oligo  
Gapop 60.0 , Gapext 60.0  
Searched: 478139 seqs, 66318000 residues

Word size: 12  
Total number of hits satisfying chosen parameters: 8  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 100 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	33.8	155	3	US-08-821-278A-17
2	32	7.0	453	3	US-08-821-278A-2
3	29	6.3	453	3	US-08-951-260A-7
4	29	6.3	453	4	US-09-430-626A-7
5	29	6.3	453	4	US-10-243-687-7
6	20	4.4	20	3	US-08-938-830-20
7	20	4.4	20	3	US-09-020-222-20
8	12	2.6	541	4	US-09-248-796A-18318

ALIGNMENTS

RESULT 1  
US-08-821-278A-17  
; Sequence 17, Application US/08821278A  
; Patent No. 6238902  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: Protein Tyrosine Phosphatases  
; FILE REFERENCE: P1010R1  
; CURRENT APPLICATION NUMBER: US/08/821,278A  
; CURRENT FILING DATE: 1997-03-20  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO 17  
; LENGTH: 155

TYPE: PRT  
ORGANISM: Homo Sapien  
US-08-821-278A-17  
Query Match 33.8%; Score 155; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 2.2e-134; Indels 0; Gaps 0;  
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 17 ARGSGEGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 76  
DB 1 ARGSGEGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 60  
QY 77 LQEBGHSDYINGNFIQVDSGLAYIATQGLPHTLLDFWLVWFEFGVKVILMACREIEN 136  
DB 61 LQEBGHSDYINGNFIQVDSGLAYIATQGLPHTLLDFWLVWFEFGVKVILMACREIEN 120  
QY 137 GSKRCERYWAQOEPLQTLGFCITILKEKWLNEDI 171  
DB 121 GSKRCERYWAQOEPLQTLGFCITILKEKWLNEDI 155

RESULT 2

US-08-821-278A-2  
; Sequence 2, Application US/08821278A  
; Patent No. 6238902  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: Protein Tyrosine Phosphatases  
; FILE REFERENCE: P1010R1  
; CURRENT APPLICATION NUMBER: US/08/821,278A  
; CURRENT FILING DATE: 1997-03-20  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO 2  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-08-821-278A-2

Query Match 7.0%; Score 32; DB 3; Length 453;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21; Indels 0; Gaps 0;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AVIATQGLPHTLLDFWLVWFEFGVKVILMAC 131  
DB 100 AVIATQGLPHTLLDFWLVWFEFGVKVILMAC 131

RESULT 3

US-08-951-260A-7  
; Sequence 7, Application US/08951260A  
; Patent No. 6004791  
; GENERAL INFORMATION:  
; APPLICANT: Aoki, Naohito  
; APPLICANT: Ullrich, Axel  
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/951,260A  
FILING DATE: October 16, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,860  
FILING DATE: No. 6004791ember 13, 1996  
APPLICATION NUMBER: PCT/1897/00946  
FILING DATE: June 17, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 227/004  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-08-951-260A-7

Query Match 6.3%; Score 29; DB 3; Length 453;  
Best Local Similarity 100.0%; Pred. NO. 2.9e-18;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGLGNLRIGRPKGRDPPAEWTRV 458  
DB 425 GAQTGGLGNLRIGRPKGRDPPAEWTRV 453

RESULT 4  
US-09-430-626A-7  
Sequence 7, Application US/09430626A  
Patent No. 6482605  
GENERAL INFORMATION:  
APPLICANT: Aoki, Naohito  
Ulrich, Axel  
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
AND RELATED PRODUCTS AND METHODS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,626A  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/951,260  
FILING DATE: October 16, 1997  
APPLICATION NUMBER: 60/030,860  
FILING DATE: No. 6482605ember 13, 1996  
APPLICATION NUMBER: PCT/1897/00946  
FILING DATE: June 17, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 227/004

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-430-626A-7  
Query Match 6.3%; Score 29; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. NO. 2.9e-18;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGLGNLRIGRPKGRDPPAEWTRV 458  
DB 425 GAQTGGLGNLRIGRPKGRDPPAEWTRV 453

RESULT 5  
US-10-243-687-7  
Sequence 7, Application US/10243687  
Patent No. 6797501  
GENERAL INFORMATION:  
APPLICANT: Aoki, Naohito  
Ulrich, Axel  
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
AND RELATED PRODUCTS AND METHODS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/243,687  
FILING DATE: 16-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,626A  
FILING DATE: 29-Oct-1999  
APPLICATION NUMBER: 08/951,260  
FILING DATE: October 16, 1997  
APPLICATION NUMBER: 60/030,860  
FILING DATE: No. 6797501ember 13, 1996  
APPLICATION NUMBER: PCT/1897/00946  
FILING DATE: June 17, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 227/004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single



TOPOLGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7;  
US-10-243-687-7

Query Match 6.3%; Score 29; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred.No. 2.9e-18;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGGFLNLRIGRPGKPRDPPAEWTRV 458  
Db 425 GAQTGGGFLNLRIGRPGKPRDPPAEWTRV 453

RESULT 6  
US-08-938-830-20  
; Sequence 20, Application US/08938830  
; Patent No. 6040437  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Laurence A.  
; APPLICANT: Dowbenko, Donald J.  
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/938,830  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/798419  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1066P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-3216  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-938-830-20

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,830  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-938-830-20

Query Match 4.4%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred.No. 3.1e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 GFNLRIGRPGKPRDPPAEWT 456  
Db 1 GFNLRIGRPGKPRDPPAEWT 20

RESULT 8  
US-09-248-796A-18318  
; Sequence 18318, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18318  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; US-09-248-796A-18318

Query Match 2.6%; Score 12; DB 4; Length 541;  
Best Local Similarity 100.0%; Pred.No. 0.014; 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0;

QY 227 VHCAGCGRTGV 238  
Db 443 VHCAGCGRTGV 454

Wed Dec 8 09:08:31 2004

us-10-087-993a-36.olig12.ra1

Page 4

Search completed: December 7, 2004, 10:00:24  
Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:55:38 ; Search time 147 Seconds  
(without alignments)  
1111.161 Million cell updates/sec

Title: US-10-087-993A-36  
Perfect score: 458  
Sequence: 1 MSRLSDARSFLERLEARGG.....NLRIGPKGPRDPAEWTRV 458

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1582225 seqs, 35663895 residues

Word size : 12

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	458	100.0	458	13 US-10-087-993-36	Sequence 36, Appl
2	29	6.3	453	14 US-10-243-687-7	Sequence 7, Appl
3	24	5.2	448	13 US-10-087-993-32	Sequence 32, Appl
4	20	4.4	20	14 US-10-340-288-13	Sequence 13, Appl
5	12	2.6	750	9 US-09-801-368-280	Sequence 280, Appl
6	12	2.6	750	14 US-10-369-493-22392	Sequence 22392, A

ALIGNMENTS

RESULT 1  
US-10-087-993-36

Sequence 36, Application US/10087993  
Publication No. US20020169303A1  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
Aoki, Naohito  
Kim, Yeong Woong  
Wang, Hong Yang  
Chen, Zhengjun  
Naylor, Oliver  
Kharitonkov, Alexei Igorevich  
TITLE OF INVENTION: NOVEL PTP20, PGP-2, BDP1, CLK,  
AND SIRP POLYPEPTIDES AND RELATED  
PRODUCTS AND METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/087,993  
FILING DATE: 05-Mar-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/877,150  
FILING DATE: June 17, 1997  
APPLICATION NUMBER: U.S. 60/019,629  
FILING DATE: June 17, 1996  
APPLICATION NUMBER: U.S. 60/023,485  
FILING DATE: August 9, 1996  
APPLICATION NUMBER: U.S. 60/030,860  
FILING DATE: No. US20020169303A1ember 13, 1996  
APPLICATION NUMBER: U.S. 60/034,286  
FILING DATE: December 19, 1996  
APPLICATION NUMBER: U.S. 60/030,964  
FILING DATE: No. US20020169303A1ember 15, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 225/298  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 458 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-10-087-993-36  
Query Match 100.0%; Score 458; DB 13; Length 458;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSRLSDARSFLERLEARGGREGAVLAGFSDIOACSAANKADGVSTVAGSRPNVRKN 60  
DB 1 MSRLSDARSFLERLEARGGREGAVLAGFSDIOACSAANKADGVSTVAGSRPNVRKN 60  
QY 61 RYKQVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAVIATQGLPHTLDDFVRLVW 120

Db 61 RYKDVLPYQTRVLSILOEGHSDYINGFIRGVDSLAYIATQGPLPHTLLEDFWLW 120  
QY 121 EFGVKVILMACRIENGRKRCRYWAQEQBPLOTGLFCITLKEKWLNEIDMLTKVTF 180  
Db 121 EFGVKVILMACRIENGRKRCRYWAQEQBPLOTGLFCITLKEKWLNEIDMLTKVTF 180  
QY 181 QKESRSVYQVQVMSVDRGVPSPDHMLAMVEEARLQSGPEPLCVCHVCSAGCGRTGVL 240  
Db 181 QKESRSVYQVQVMSVDRGVPSPDHMLAMVEEARLQSGPEPLCVCHVCSAGCGRTGVL 240  
QY 241 TVDYVQQLLTQVMPDFSLFDVLLKORQORPAAVQTEQYRFLYHTVAQMFCSLTQNAS 300  
Db 241 TVDYVQQLLTQVMPDFSLFDVLLKORQORPAAVQTEQYRFLYHTVAQMFCSLTQNAS 300  
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPFGVLRISVPSGPGHAMADTYAEQKR 360  
Db 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPFGVLRISVPSGPGHAMADTYAEQKR 360  
QY 361 GAPAGAGSGTGTGTGARSASEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADQSPAG 420  
Db 361 GAPAGAGSGTGTGTGARSASEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADQSPAG 420  
QY 421 SGAYEDVAGAGTGGGLGFNLRIGRPKGRDPPAEWTRV 458  
Db 421 SGAYEDVAGAGTGGGLGFNLRIGRPKGRDPPAEWTRV 458

## RESULT 2

US-10-243-687-7  
; Sequence 7, Application US/10243687  
; Publication No. US20030073120A1

## GENERAL INFORMATION:

APPLICANT: Aoki, Naohito

Ulrich, Axel

TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
AND RELATED PRODUCTS AND METHODS

## NUMBER OF SEQUENCES: 7

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

## COMPUTER:

IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/243,687

FILING DATE: 16-Sep-2002

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/430,626A

FILING DATE: 29-Oct-1999

APPLICATION NUMBER: 08/951,260

FILING DATE: October 16, 1997

APPLICATION NUMBER: 60/030,860

FILING DATE: No. US20030073120A1ember 13, 1996

APPLICATION NUMBER: PCT/1897/00946

FILING DATE: June 17, 1997

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 227/004

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-243-687-7

## Query Match

Best Local Similarity 6.3%; Score 29; DB 14; Length 453;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGGLGFNLRIGRPKGRDPPAEWTRV 458

Db 425 GAQTGGGLGFNLRIGRPKGRDPPAEWTRV 453

## RESULT 3

US-10-087-993-32

; Sequence 32, Application US/10087993

; Publication No. US20020169303A1

## GENERAL INFORMATION:

APPLICANT: Ulrich, Axel

Aoki, Naohito

Kim, Yeong Woong

Wang, Hong Yang

Chen, Zhengjun

Naylor, Oliver

Kharitonov, Alexei Igorevich

TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPI, CLK,  
AND SIRP POLYPEPTIDES AND RELATED

PRODUCTS AND METHODS

## NUMBER OF SEQUENCES: 38

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

## COMPUTER:

IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/087,993

FILING DATE: 05-Mar-2002

CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/877,150

FILING DATE: June 17, 1997

APPLICATION NUMBER: U.S. 60/019,629

FILING DATE: June 17, 1996

APPLICATION NUMBER: U.S. 60/023,485

FILING DATE: August 9, 1996

APPLICATION NUMBER: U.S. 60/030,860

FILING DATE: No. US20020169303A1ember 13, 1996

APPLICATION NUMBER: U.S. 60/034,286

FILING DATE: December 19, 1996

APPLICATION NUMBER: U.S. 60/030,964

FILING DATE: No. US20020169303A1ember 15, 1996

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 225/298

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-10-087-993-32

Query Match 5.2%; Score 24; DB 13; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLEPHTLLDFWRLWVEFG 123  
DB 100 AYIATQGPLEPHTLLDFWRLWVEFG 123

RESULT 4  
US-10-340-288-13  
; Sequence 13, Application US/10340288  
; Publication No. US20030170855A1  
; GENERAL INFORMATION:  
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University  
; APPLICANT: ZHANG, Zhong-Yin  
; APPLICANT: XIE, Laiping  
; APPLICANT: ZHANG, Yan-Ling  
; TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE PHOSPHATASE SUBSTRATE-TRAPPING DOUBLE  
; TITLE OF INVENTION: MUTANT AND USES THEREOF  
; FILE REFERENCE: 96700/792  
; CURRENT APPLICATION NUMBER: US/10/340,288  
; PRIOR FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: US 60/347,413  
; PRIOR FILING DATE: 2002-01-17  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 13  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-340-288-13

Query Match 4.4%; Score 20; DB 14; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 VVLKMKRQRPAAVQTEEQYR 282  
DB 1 VVLKMKRQRPAAVQTEEQYR 20

RESULT 5  
US-09-801-368-280  
; Sequence 280, Application US/09801368  
; Patent No. US20020128250A1  
; GENERAL INFORMATION:  
; APPLICANT: Busby, Robert  
; APPLICANT: Cali, Brian  
; APPLICANT: Hecht, Peter  
; APPLICANT: Holtzman, Doug  
; APPLICANT: Madden, Kevin  
; APPLICANT: Maxon, Mary  
; APPLICANT: Milne, Todd  
; APPLICANT: No. US20020128250Alman, Thea  
; APPLICANT: Royer, John  
; APPLICANT: Salama, Sofie  
; APPLICANT: Sherman, Amir  
; APPLICANT: Silva, Jeff  
; APPLICANT: Summers, Eric  
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
; FILE REFERENCE: 109272.147  
; CURRENT APPLICATION NUMBER: US/09/801,368

CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 09/487,558  
PRIOR FILING DATE: 2000-01-19  
PRIOR APPLICATION NUMBER: US 60/160,587  
PRIOR FILING DATE: 1999-10-20  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 280  
LENGTH: 750  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
US-09-801-368-280

Query Match 2.6%; Score 12; DB 9; Length 750;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCSAGCGRTGV 238  
DB 664 VHCSAGCGRTGV 675

RESULT 6  
US-10-369-493-22392  
; Sequence 22392, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22392  
; LENGTH: 750  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-22392

Query Match 2.6%; Score 12; DB 14; Length 750;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCSAGCGRTGV 238  
DB 664 VHCSAGCGRTGV 675

Search completed: December 7, 2004, 10:02:57  
Job time: 147 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:53:48 ; Search time 19 Seconds  
(without alignments)  
2319.330 Million cell updates/sec

Title: US-10-087-993A-36  
Perfect score: 458  
Sequence: 1 MSRLSDARSFLERLARGS.....NLRIQPKGPRDPPAEWTRV 458

Scoring table: OLIGO 2  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 12 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR 79:.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	2.6	750	2	protein-tyrosine-p

ALIGNMENTS

RESULT 1  
S67100  
protein-tyrosine-phosphatase (EC 3.1.1.3.48) PTP2 - yeast (Saccharomyces cerevisiae)  
N/Alternate names: protein 04849; protein YOR208w  
C/Species: Saccharomyces cerevisiae  
C/Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 09-Jul-2004  
C/Accession: S67100; A42667; A41980; S31554; S14170; JCI484; S42155  
R/Hughes, B.; Pohl, T.M.  
submitted to the Protein Sequence Database, July 1996  
A/Reference number: S66685  
A/Accession: S67100  
A/Molecule type: DNA  
A/Residues: 1-750 <HUG>  
A/Cross-references: UNIPROT:P29461; EMBL:Z75116; NID:G1420486; PID:e252394; PID:G1420487  
A/Experimental source: strain S288C  
J. Biol. Chem. 267, 10024-10030, 1992  
A/Title: Isolation and characterization of a second protein tyrosine phosphatase gene, P  
A/Reference number: A42667; MUID:92250559; PMID:1577774  
A/Accession: A42667  
A/Molecule type: DNA  
A/Residues: 1-473, 'NV', 476-750 <GUA>  
A/Cross-references: GB:M85287

R/Ota, I.M.; Varshavsky, A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2355-2359, 1992  
A/Title: A gene encoding a putative tyrosine phosphatase suppresses lethality of an N-ent  
A/Reference number: A41980; MUID:92196117; PMID:1549598  
A/Accession: A41980  
A/Molecule type: DNA  
A/Residues: 1-750 <OTA>  
A/Cross-references: EMBL:M82872; NID:G172293; PID:AAA34922.1; PID:G172294  
A/Note: sequence extracted from NCBI backbone (NCBIN:88405, NCBI:P:88407)  
R/James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.  
submitted to the EMBL Data Library, July 1991  
A/Description: Multiple protein tyrosine phosphatase-encoding genes in the yeast Sacchar  
A/Reference number: S31554  
A/Accession: S31554  
A/Molecule type: DNA  
A/Residues: 1-370, 'S', 372-659, 'GA', 662-750 <JAM>  
A/Cross-references: EMBL:M38723; NID:G172381; PID:G172382  
R/James, P.; Whelen, S.; Hall, B.D.  
J. Biol. Chem. 266, 5616-5624, 1991  
A/Title: The RET1 gene of yeast encodes the second-largest subunit of RNA polymerase III  
A/Reference number: S14169; MUID:91170230; PMID:2005101  
A/Accession: S14170  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-67 <JBI>  
A/Cross-references: EMBL:M38723  
R/James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.  
Gene 122, 101-110, 1992  
A/Title: Multiple protein tyrosine phosphatase-encoding genes in the yeast Saccharomyces  
A/Reference number: JCI484; MUID:93083970; PMID:1452018  
A/Accession: JCI484  
A/Molecule type: DNA  
A/Residues: 1-370, 'S', 372-659, 'GA', 662-750 <JAW>  
C/Genetics:  
A/Gene: SGD:PTP2  
A/Cross-references: SGD:S0005734; MIPS:YOR208w  
A/Map position: 15R  
C/Keywords: cell division control; nucleotide binding; phosphoprotein; phosphoric monoos  
F/408-726/Domain: protein-tyrosine-phosphatase homology <Ptp>  
F/669-674/Region: nucleotide binding #status predicted  
F/666/Active site: Cys (phosphocysteine intermediate) #status predicted  
F/672/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 12; DB 2; Length 750;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCAGCGRTGV 238  
|||  
Db 664 VHCAGCGRTGV 675

Search completed: December 7, 2004, 09:59:57  
Job time : 20 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:50:28 ; Search time 77 Seconds  
(without alignments)  
3422.358 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458  
Sequence: 1 MSRLSDSARSFLERLEARGG.....NLRIKPKGRPPPAEWTRV 458

Scoring table: OLIGO)  
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size: 12

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_tramb1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	458	100.0	458	1 PTNI HUMAN	Q99952 homo sapien
2	217	47.4	351	2 Q7Z637	Q7Z637 homo sapien
3	217	47.4	372	2 Q6TA96	Q6TA96 homo sapien
4	32	7.0	453	2 Q61152	Q61152 mus musculus
5	32	7.0	453	2 Q922B3	Q922B3 mus musculus
6	29	6.3	453	2 P70602	P70602 rattus norv
7	12	2.6	258	2 Q90Y62	Q90Y62 brachydanio
8	12	2.6	487	2 Q9NL13	Q9NL13 brachydanio
9	12	2.6	570	2 Q6PE14	Q6PE14 brachydanio
10	12	2.6	570	2 RAH58051	RAH58051 brachydan
11	12	2.6	572	2 Q6NZ14	Q6NZ14 brachydanio
12	12	2.6	572	2 AAH66385	AAH66385 brachydan
13	12	2.6	684	2 Q6FLK0	Q6FLK0 candida gla
14	12	2.6	750	1 PTP2 YEAST	P29461 saccharomyc
15	12	2.6	799	2 Q75BW3	Q75BW3 ashbya goss
16	12	2.6	799	2 RA551384	RA551384 ashbya go
17	12	2.6	903	2 Q6CR74	Q6CR74 kluyveromyc

ALIGNMENTS

ID	PTNI_HUMAN	STANDARD;	PRT;	458 AA.
AC	Q99952;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)			
DE	(Brain-derived phosphatase).			

RESULT 1

GN	Name=PTPN18; Synonyms=BDP1;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.
RC	TISSUE=Brain;
RX	MEDLINE=97108674; PubMed=8950995;
RA	Kim Y.W., Wang H.Y., Sures I., Lammers R., Martell K.J., Ullrich A.;
RT	"Characterization of the PEST family protein tyrosine phosphatase
RT	BDP1.";
RL	Oncogene 13:2275-2279(1996)
CC	!-FUNCTION: Differentially dephosphorylate autophosphorylated
CC	tyrosine kinases which are known to be overexpressed in tumor
CC	tissues.
CC	!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC	tyrosine + phosphate.
CC	!- TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-
CC	derived cell lines.
CC	!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC	Non-receptor class 4 subfamily.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X79568; CAA56105.1; -
DR	HSSP; Q66124; 2SHP.
DR	Genew; HGNC:9649; PTPN18.
DR	MIM; 606587; -
DR	GO; GO:0004726; F:non-membrane spanning protein tyrosine phosph. .; TAS.
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR	InterPro; IPR000387; TYR_PTP.
DR	InterPro; IPR000242; TYR_PP.
DR	Fam; PF00102; Y_PTPase; 1.
DR	PRINTS; PR00700; PRTYPHPTASE.
DR	SMART; SM00194; PTPC; 1.
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW	Hydrolase; Protein phosphatase.
FT	DOMAIN 26 291 Protein-tyrosine phosphatase. (By
FT	ACT_SITE 229 229 Phosphocysteine intermediate similarity).
SQ	SEQUENCE 458 AA; 50384 MW; 46BCA1E17C2C78B1 CRC64;
Query Match	
Best Local Similarity 100.0%; Score 458; DB 1; Length 458;	
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSRLSDSARSFLERLEARGGREGAVLAGEFSDIQACSAAKADGVCSIVAGSRPENVRKN 60
Db	1 MSRLSDSARSFLERLEARGGREGAVLAGEFSDIQACSAAKADGVCSIVAGSRPENVRKN 60
QY	61 RYKQVLPDQTRVILSLQEGHSDYINGNIRGVDSGLAYIATQGPLHTLLDFWRLVW 120
Db	61 RYKQVLPDQTRVILSLQEGHSDYINGNIRGVDSGLAYIATQGPLHTLLDFWRLVW 120
QY	121 EFGVKVILMACREIENGKRCERYWAQOEPLQGLFCITLIKELNEDIMRLTKVTF 180
Db	121 EFGVKVILMACREIENGKRCERYWAQOEPLQGLFCITLIKELNEDIMRLTKVTF 180
QY	181 QKESRSVYQLQYMSWPDGVPSSPDHMLAMVEARRLQSGSGPEPLCVHCSAGCGTGVLC 240
Db	181 QKESRSVYQLQYMSWPDGVPSSPDHMLAMVEARRLQSGSGPEPLCVHCSAGCGTGVLC 240
QY	241 TVDYVQRLTLTQWIPDPSLFDVVLKMKQRPAAVQTEEQYRFLYHTVAQMFCSLQNAS 300

Db 241 TVDYVRLQLLTQMIPDPFSLFDVVLKMKRQPAAVQTEQRYFLYHTVAQWFCSTLQNAS 300  
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLSISVPGSPGHAMADTYVAEQKR 360  
 Db 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLSISVPGSPGHAMADTYVAEQKR 360  
 QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAQPCAHAEADARGTLPGRVPADQSPAG 420  
 Db 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAQPCAHAEADARGTLPGRVPADQSPAG 420  
 QY 421 SGAYEDVAGGAQTGGLGNLRIGRPGKPRDPPAEWTRV 458  
 Db 421 SGAYEDVAGGAQTGGLGNLRIGRPGKPRDPPAEWTRV 458

RESULT 2

Q72637 PRELIMINARY; PRT; 351 AA.

AC Q72637; (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 26, Last annotation update)  
 DE PTPN18 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.A., Lomellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC052800; AAH52800.1; -;  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR SMART; SM00194; PTPc; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolase. 351 AA; 38317 MW; 5FE9B48C5D0667C4 CRC64;  
 SQ SEQUENCE 351 AA; 38317 MW; 5FE9B48C5D0667C4 CRC64;

Query Match 47.4%; Score 217; DB 2; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 1e-207;  
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAQCEPLQGLFCITLIKELKWLNEIMLRLTKVTFQKESRSVYQLQYMSWPD 198  
 Db 32 KRCERYWAQCEPLQGLFCITLIKELKWLNEIMLRLTKVTFQKESRSVYQLQYMSWPD 91  
 QY 199 GVPSSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRLQLLTQMIPDP 258  
 Db 92 GVPSSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRLQLLTQMIPDP 151  
 QY 259 SLFDVVLKMKRQPAAVQTEQRYFLYHTVAQWFCSTLQNASPHYQNIKENCAPLYDDAL 318  
 Db 152 SLFDVVLKMKRQPAAVQTEQRYFLYHTVAQWFCSTLQNASPHYQNIKENCAPLYDDAL 211  
 QY 319 FLRTPOALLAI PRPPGGVLSISVPGSPGHAMADTYA 355  
 Db 212 FLRTPOALLAI PRPPGGVLSISVPGSPGHAMADTYA 248

RESULT 3

Q8TA96 PRELIMINARY; PRT; 372 AA.

AC Q8TA96; (T-EMBLrel. 21, Created)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Similar to protein tyrosine phosphatase, non-receptor type 18 (Brain-  
 DE derived) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC024280; AAH24280.1; -;  
 DR EMBL; BC041562; AAH41562.1; -;  
 DR HSP; P18031; IC88.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0004725; F:receptor activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00102; Y\_phosphatase; 1.  
 DR PRINTS; PR00700; PTPPHFIAS.  
 DR SMART; SM00194; PTPc; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolase, receptor.  
 FT NON\_TER 1  
 SQ SEQUENCE 372 AA; 40708 MW; 417CA80AA054CF8B CRC64;

Query Match 47.4%; Score 217; DB 2; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-207;  
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAQCEPLQGLFCITLIKELKWLNEIMLRLTKVTFQKESRSVYQLQYMSWPD 198  
 Db 53 KRCERYWAQCEPLQGLFCITLIKELKWLNEIMLRLTKVTFQKESRSVYQLQYMSWPD 112  
 QY 199 GVPSSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRLQLLTQMIPDP 258  
 Db 113 GVPSSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVRLQLLTQMIPDP 172  
 QY 259 SLFDVVLKMKRQPAAVQTEQRYFLYHTVAQWFCSTLQNASPHYQNIKENCAPLYDDAL 318

Db 173 SLFDVVKWEKQRPAAVQEEQRELYHTVAQWFCSTLQNASPHYQNKENCAPLYDDAL 232  
Qy 319 FLRTPQALLAIPRPGVLRISIVPGSGHAMADTYA 355  
Db 233 FLRTPQALLAIPRPGVLRISIVPGSGHAMADTYA 269  
RESULT 4  
Q61152 PRELIMINARY; PRT; 453 AA.  
ID Q61152 Q62404;  
AC Q61152; Q62404;  
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCE).  
DE Name=Ptpn18; Synonyms=Ptpk1;  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=EMBRIO;  
RX MEDLINE=96329547; PubMed=8695832;  
RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;  
RT "A novel protein tyrosine phosphatase expressed in  
RL lin(CD34(hi)Sca(hi)) hematopoietic progenitor cells.";  
RN Blood 88:1156-1167(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RX MEDLINE=97030045; PubMed=8875997;  
RA Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.;  
RT "Cloning and characterization of PTP-K1, a novel nonreceptor protein tyrosine phosphatase highly expressed in bone marrow";  
RN Oncogene 13:1567-1573(1996).  
RN [3]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC STRAIN=C57BL/6; TISSUE=FETAL LIVER;  
RX MEDLINE=97131769; PubMed=8977243;  
RA Dosil M., Leibman N., Lemischka I.R.;  
RT "Cloning and characterization of fetal liver phosphatase 1, a nuclear protein tyrosine phosphatase isolated from hematopoietic stem cells.";  
RN Blood 88:4510-4525(1996).  
CC -!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF HEMATOPOIETIC CELLS.  
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN  
CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=FLP1A;  
CC IsoId=Q61152-1; Sequence=Displayed;  
CC Name=FLP1B;  
CC IsoId=Q61152-2; Sequence=VSP 050405;  
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO  
CC EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.  
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-  
CC TYROSINE PHOSPHATASE FAMILY.  
DR EMBL; U35124; AAB82736.1; -;  
DR EMBL; U49853; AAB18623.1; -;  
DR EMBL; U52523; AAC52991.1; -;  
DR HSSP; Q06124; 2SHP.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . . ; IDA.  
DR InterPro; IPR000387; TYR\_PP.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPHPHTASE.

DR SMART; SMO0194; PTPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
DR PROSITE; PS0056; TYR\_PHOSPHATASE 2; 1.  
DR PROSITE; PS0055; TYR\_PHOSPHATASE\_PTP; 1.  
KW Alternative splicing; Hydrolase; Nuclear protein.  
FT DOMAIN 56 290 PROTEIN-TYROSINE PHOSPHATASE.  
FT DOMAIN 312 428 PRO/SER/THR-RICH.  
FT ACT\_SITE 229 229 BY SIMILARITY.  
FT VARSPLIC 9 32 Missing (in isoform FLP1B).  
FT FTId=VSP 050405.  
FT CONFLICT 11 11 F -> L (IN REF. 3).  
FT CONFLICT 362 368 ASACTGP -> LRRHRA (IN REF. 3).  
SQ SEQUENCE 453 AA; 50201 MW; 89AD7E73CE8136B0 CRC64;  
Query Match 7.0%; Score 32; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.1e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 100 AYIATQGPLPHTLLDFWELVWVFGVKVILMAC 131  
DB 100 AYIATQGPLPHTLLDFWELVWVFGVKVILMAC 131  
RESULT 5  
Q922E3 PRELIMINARY; PRT; 453 AA.  
ID Q922E3  
AC Q922E3  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Ptpn18 protein.  
GN Name=Ptpn18;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II;  
RX TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Diachenko L., Marusina K., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II;  
RX TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
RA Strausberg R.L. (2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC008512; AAB08512.1; -;  
DR HSSP; Q06124; 2SHP.  
DR MGD; MGI:108410; Ptpn18.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . . ; IDA.

DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.  
SQ SEQUENCE 453 AA; 50227 MW; 722FDE1FFC9F4689 CRC64;  
  
Query Match 7.0%; Score 32; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.1e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 100 AYIATQGPPLTLLDFWRLVWVFGVKVILMAC 131  
DB 100 AYIATQGPPLTLLDFWRLVWVFGVKVILMAC 131  
  
RESULT 6  
P70602 PRELIMINARY; PRT; 453 AA.  
AC P70602;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Protein tyrosine phosphatase 20.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97067206; PubMed=8910608;  
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;  
EMBL; U69673; AAC52896.1; -.  
DR HSP; Q06124; 2SHP.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase.  
SQ SEQUENCE 453 AA; 50106 MW; 6CCC132206FB69AE CRC64;  
  
Query Match 6.3%; Score 29; DB 2; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 430 GAQTGGGLGNLRIGRPGKGRDPPAEWTRV 458  
DB 425 GAQTGGGLGNLRIGRPGKGRDPPAEWTRV 453  
  
RESULT 7  
Q90Y62 PRELIMINARY; PRT; 258 AA.  
AC Q90Y62;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Receptor PTP-like protein IA-2 (Fragment).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OC NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21076097; PubMed=11206415;  
RA Cai T., Krause M.W., Odenwald W.F., Toyama R., Notkins A.L.;  
RT "The IA-2 gene family: homologs in Caenorhabditis elegans, Drosophila  
and zebrafish."; 81-88 (2001).  
RL Diabetologia 44:81-88 (2001).  
DR EMBL; AF190144; AAL05974.1; -.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00194; PTPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 1.  
KW Hydrolase; Receptor.  
FT NON\_TER 1  
SQ SEQUENCE 258 AA; 29544 MW; 93FEC53CAA4EA4A2 CRC64;  
  
Query Match 2.6%; Score 12; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 100 AYIATQGPPLPHT 111  
DB 58 AYIATQGPPLPHT 69  
  
RESULT 8  
Q9NLI3 PRELIMINARY; PRT; 487 AA.  
AC Q9NLI3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE APTPR4c protein (Fragment).  
GN Name=amPTPR4c;  
OS Branchiostoma belcheri (Amphioxus).  
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
OC Branchiostoma.  
OC NCBI\_TaxID=7741;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20219325; PubMed=10754074;  
RA Ono K., Koyanagi K., Suga H., Katoh K., Miyata T.;  
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
divergence of tissue-specific isoform genes in the early evolution of  
vertebrates."; 50:302-311 (2000).  
RL J. Mol. Evol. 50:302-311 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Ono K.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB033564; BAA95171.1; -.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00102; Y\_phosphatase; 2.

DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SMO0194; PTPC; 2.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase.  
SQ SEQUENCE 487 AA; 55573 MW; CF2BCCDD933C6ADD CRC64;  
Query Match 2.6%; Score 12; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
FT NON\_TER 1 1  
SQ SEQUENCE 487 AA; 55573 MW; CF2BCCDD933C6ADD CRC64;  
Query Match 2.6%; Score 12; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 100 AYIATQGLPHT 111  
DB 267 AYIATQGLPHT 278  
RESULT 9  
ID Q6PEI4 PRELIMINARY; PRT; 570 AA.  
AC Q6PEI4  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Protein tyrosine phosphatase, non-receptor type 12.  
GN Name:ptp12;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC058051; AAH58051.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003595; PTPC motif.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_Pp.  
DR Pfam; PF00102; Y\_phosphatase; 1.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SMO0194; PTPC; 1.  
DR SMART; SMO0404; PTPC motif; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 1.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 1.

KW Hydrolase; Receptor.  
SQ SEQUENCE 570 AA; 64502 MW; 19D2959BEF5F02B CRC64;  
Query Match 2.6%; Score 12; DB 2; Length 570;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 226 CVHCSAGCGRTG 237  
DB 225 CVHCSAGCGRTG 236  
RESULT 10  
AAH58051 PRELIMINARY; PRT; 570 AA.  
ID AAH58051  
AC AAH58051  
DT 24-MAY-2004 (TREMBlrel. 27, Created)  
DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)  
DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)  
DE Protein tyrosine phosphatase, non-receptor type 12.  
GN PTPN12.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC058051; AAH58051.1; -;  
DR KX Receptor.  
SQ SEQUENCE 570 AA; 64502 MW; 19D2959BEF5F02B CRC64;  
Query Match 2.6%; Score 12; DB 2; Length 570;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 226 CVHCSAGCGRTG 237  
DB 225 CVHCSAGCGRTG 236  
RESULT 11  
Q6NZ14 PRELIMINARY; PRT; 572 AA.  
ID Q6NZ14  
AC Q6NZ14  
DT 05-JUL-2004 (TREMBlrel. 27, Created)



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RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR380958; CAG61864.1; -.
DR InterPro; IPR003595; Pfam; P00102; Y_PTYPHPTASE.
DR InterPro; IPR000387; Tyr_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_PTYPHPTASE.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ
SEQUENCE 684 AA; 78640 MW; CAPBB6EC6B2D23E CRC64;

Query Match 2.6%; Score 12; DB 2; Length 684;
Best Local Similarity 100.0%; Pred.No. 0.016; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 227 VHCAGCGRTGV 238
DB 596 VHCAGCGRTGV 607
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RESULT 14
PTP2_YEAST STANDARD; PRT; 750 AA.
AC P294G;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase 2 (EC 3.1.3.48) (PTPase 2).
GN Name=PTP2; OrderedLocustNames=YOR208W;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RZ SEQUENCE FROM N.A.
RX MEDLINE=92196117; PubMed=1577774;
RA Guan K., Deschenes R.J., Dixon J.E.;
RT "Isolation and characterization of a second protein tyrosine phosphatase gene, PTP2, from Saccharomyces cerevisiae.";
RL J. Biol. Chem. 267:10024-10030 (1992).
RN [2]
RZ SEQUENCE FROM N.A.
RX MEDLINE=92196117; PubMed=1549598;
RA Ota I.M., Varshavsky A.;
RT "A gene encoding a putative tyrosine phosphatase suppresses lethality of an N-end rule-dependent mutant.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2355-2359 (1992).
RN [3]
RZ SEQUENCE FROM N.A.
RX James P., Hall B.D., Whelen S., Craig E.A.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RZ SEQUENCE FROM N.A.
RX Hughes B., Pohl T.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be implicated in the ubiquitin-mediated protein degradation pathway. May be involved in the regulation of MAP kinase FUS3.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily.
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CC or send an email to license@isb-sib.ch).
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CC EMBL; M85287; -. NOT ANNOTATED_CDS.
DR EMBL; M82872; AAA34922.1; -.
DR EMBL; M38723; AAB59323.1; -.
DR EMBL; Z75116; CAA99423.1; -.
DR PIR; S67100; S67100.
DR HSSP; P18052; 1YFO.
DR GerMOnline; 143796; -.
DR SGD; S0005734; PTP2.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR000387; Tyr_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_PTYPHPTASE.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Protein phosphatase.
KW ACT_SITE 666
FT Phosphotyrosine intermediate (By similarity).
FT CONFLICT 371 371 L -> S (in Ref. 3).
FT CONFLICT 474 475 KL -> NV (in Ref. 1).
FT CONFLICT 660 661 SP -> GA (in Ref. 3).
SQ SEQUENCE 750 AA; 85868 MW; 1033D2F0AA23BD35 CRC64;

Query Match 2.6%; Score 12; DB 1; Length 750;
Best Local Similarity 100.0%; Pred.No. 0.017; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 227 VHCAGCGRTGV 238
DB 664 VHCAGCGRTGV 675
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RESULT 15
Q75BW3 PRELIMINARY; PRT; 799 AA.
AC Q75BW3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ACR158WP.
GN Name=ACR158W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OC NCBI_TaxID=33169;
RN [1]
RZ SEQUENCE FROM N.A.
RX STRAIN=ATCC 10895;
RX PubMed=15001715;
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A., Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
RL Science 304:304-307 (2004)
DR EMBL; A5016888; AAS51384.1; -.
DR AGD; ACR158W; -.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; Tyr_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_PTYPHPTASE; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.

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KW PROSITE; PSS0055; TYR\_PHOSPHATASE\_PTP; 1.

KR Hydrolase. 799 AA; 89345 MW; A619E56C3C969640 CRC64;

SQ SEQUENCE 799 AA; 89345 MW; A619E56C3C969640 CRC64;

Query Match 2.6%; Score 12; DB 2; Length 799;  
Best Local Similarity 100.0%; Pred.No. 0.018;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCSAGCGRTGV 238

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DB 713 VHCSAGCGRTGV 724

RESULT 16

AAS51384

ID AAS51384 PRELIMINARY; PRT; 799 AA.

AC AAS51384;

DT 23-APR-2004 (TREMELrel. 27, Created)

DT 23-APR-2004 (TREMELrel. 27, Last sequence update)

DT 23-APR-2004 (TREMELrel. 27, Last annotation update)

DE ACR158Wp.

GN ACR158W.

OS Ashbya gossypii (Yeast) (Eremothecium gossypii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Eremothecium.

OX NCBI\_TaxID=33169;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 10895;

RX PubMed=15001715;

RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,

RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavien A.,

RA Gaffney T.D., Philippsen P.;

RT "The Ashbya gossypii genome as a tool for mapping the ancient

RT Saccharomycetes cerevisiae genome.";

RL Science 304:304-307(2004).

DR EMBL; AF016888; AAS51384.1; "

SQ SEQUENCE 799 AA; 89345 MW; A619E56C3C969640 CRC64;

Query Match

Best Local Similarity 100.0%; Pred.No. 0.018;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCSAGCGRTGV 238

|||||

DB 713 VHCSAGCGRTGV 724

RESULT 17

Q6CRT4

ID Q6CRT4 PRELIMINARY; PRT; 903 AA.

AC Q6CRT4;

DT 01-OCT-2004 (TREMELrel. 28, Created)

DT 01-OCT-2004 (TREMELrel. 28, Last sequence update)

DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)

DE Strain NRRL Y-1140 chromosome D of strain NRRL Y-1140 of Kluyveromyces

DE lactis.

GN ORFNames=KLLA0D06611g;

OS Kluyveromyces lactis (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI\_TaxID=28985;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRRL Y-1140;

RG GENOLEVURES;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talia E.,

RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,

RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pallenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Svennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts.";

RL Nature 430:35-44(2004).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NRRL Y-1140;

RA Genoscope;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR382124; CAH00451.1; "

SQ SEQUENCE 903 AA; 102110 MW; 5E71496FAE5D6197 CRC64;

Query Match 2.6%; Score 12; DB 2; Length 903;

Best Local Similarity 100.0%; Pred.No. 0.02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCSAGCGRTGV 238

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DB 823 VHCSAGCGRTGV 834

Search completed: December 7, 2004, 09:59:33

Job time : 78 secs